

1	2323.4	99.9	2325	2	AX644009	Sequence
2	2320.6	99.8	2340	5	AF488550	Homo sapi
3	2320.2	99.8	3852	2	AX686997	Sequence
4	2133.2	91.8	3522	5	AB040968	Homo sapi
5	2122.6	91.3	2976	2	AR542069	Sequence
6	2122.6	91.3	2976	2	AX699231	Sequence
7	2110.4	90.8	3496	2	AX348090	Sequence
8	1876.2	80.7	3226	6	BC039156	Mus muscu
9	1876.2	80.7	3268	6	BC0325124	Mus muscu
10	1872.8	80.6	2343	6	AF247452	Rattus no
11	1712.2	73.6	3454	5	BC000066	Homo sapi
12	1638.8	70.5	3245	5	BC005840	Homo sapi
13	1343.4	57.8	2756	5	BC028024	Homo sapi
14	1131.4	48.7	3737	14	AB022927	Oryctolag
15	1087.4	46.8	4751	2	AX019005	Sequence
16	1085.8	46.7	4751	2	AX348088	Sequence
17	1085.8	46.7	4751	5	HS238850	Homo sapi
18	1085.8	46.7	5065	2	AX211348	Sequence
19	1085.8	46.7	5065	2	AX211348	Homo sapi
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24	1085.8	46.7	5065	2	AX211348	Sequence
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28	1085.8	46.7	5065	2	AX211348	Sequence
29	1085.8	46.7	5065	2	AX211348	Homo sapi
30	1085.8	46.7	5065	2	AX211348	Sequence
31	1085.8	46.7	5065	2	AX211348	Homo sapi
32	1085.8	46.7	5065	2	AX211348	Sequence
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34	1085.8	46.7	5065	2	AX211348	Sequence
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42	1085.8	46.7	5065	2	AX211348	Sequence
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46	1085.8	46.7	5065	2	AX211348	Sequence
47	1085.8	46.7	5065	2	AX211348	Homo sapi
48	1085.8	46.7	5065	2	AX211348	Sequence
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58	1085.8	46.7	5065	2	AX211348	Sequence
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63	1085.8	46.7				

181 TCCCTTCGGGTGTTTCGGACGCCAAGCAGTGGAAATCGAGCAGGAGGGGTGAAGTCA 240
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 241 GCGGGGCTCGATCATCAACCTTACAGGACCTTCGGGTTTATCGGACCTGATCATG 300
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 301 CTGCTGCTGATGTGGGGAACCTCATCGTCTCCCTGCTGGGCATCACTTCTCAAGGAG 360
 361 GAGAACTCCCGCTTGGATCGTCTTCAAGTATGTCTGATATCTTCTCTACTGGAT 420
 361 GAGAACTCCCGCTTGGATCGTCTTCAAGTATGTCTGATATCTTCTCTACTGGAT 420
 421 CTGGTGTCAACTTCGGAACGGGCATCGTGGTGGAGAGGGTCTGAGATCTCTGTCGCA 480
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 481 CCGGGGCTCATCGCAGCGCTACCTCGGCACATGTTCTGCTGCTGCTGCTCTCTCT 540
 481 CCGGGGCTCATCGCAGCGCTACCTCGGCACATGTTCTGCTGCTGCTGCTCTCTCTCT 540
 541 ATCCCTGTGGATTAACATCTTCTTAGTGGAGCTGGAGCCACGGTTGGACGCTGAGGTC 600
 541 ATCCCTGTGGATTAACATCTTCTTAGTGGAGCTGGAGCCACGGTTGGACGCTGAGGTC 600
 601 TACAAAACGGCAGCGGCTTACGATCTGTTGCTTCAACAGATCTTCAAGCTCTGAGG 660
 601 TACAAAACGGCAGCGGCTTACGATCTGTTGCTTCAACAGATCTTCAAGCTCTGAGG 660
 661 CTGCTCGGCTCTCCCGCTCATCGCTACATACACAGTGGAGGAGATCTTCAATG 720
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 721 ACCTATGACCTGCGCAGTGTGTTGCTGATCTTCAACCTCATTTGGATGATGCTGCTG 780
 721 ACCTATGACCTGCGCAGTGTGTTGCTGATCTTCAACCTCATTTGGATGATGCTGCTG 780
 781 CTATGCTACGAGTGGCTGTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 781 CTATGCTACGAGTGGCTGTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 841 GACTGTGCTGCTTCAATCAACACATGTTGAACTCTGTTGGGCGCGCAGTATTCCTAT 900
 841 GACTGTGCTGCTTCAATCAACACATGTTGAACTCTGTTGGGCGCGCAGTATTCCTAT 900
 901 GGCCTGTTCAAGGCCATGAGCCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 901 GGCCTGTTCAAGGCCATGAGCCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
 961 GGCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
 961 GGCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
 1021 ATGTTTCAATGCGGCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 1021 ATGTTTCAATGCGGCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
 1081 CAGGAGAAGTACAAGCAGGTGGAGCAGTATGCTTCTTCCAAAGTGTGCGCAGACACG 1140
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 1141 CCGCAGCGCATCAAGTATGAGCAACGCTTACAGGCAAGATGTTTCATGAGGAA 1200
 1141 CCGCAGCGCATCAAGTATGAGCAACGCTTACAGGCAAGATGTTTCATGAGGAA 1200
 1201 AGCATCTGGGAGCTGAGCGGCTTCCGAGGAGATCATTAACCTTCACTGCTGCG 1260
 1201 AGCATCTGGGAGCTGAGCGGCTTCCGAGGAGATCATTAACCTTCACTGCTGCG 1260

QY 1261 GCGCTGTGGGCCACATGCGCTGTTTGGCCATGCGCAGACCCAGCTTCGTCACTGCACTT 1320
 DB 1261 GCGCTGTGGGCCACATGCGCTGTTTGGCCATGCGCAGACCCAGCTTCGTCACTGCACTT 1320
 QY 1321 CTCACAAAGCTGCGCTTTGAGGCTTTCAGCGCGGGGAGATCTCGTGGTGGTGAAGGCTCC 1380
 DB 1321 CTCACAAAGCTGCGCTTTGAGGCTTTCAGCGCGGGGAGATCTCGTGGTGGTGAAGGCTCC 1380
 QY 1381 GTGGGGAGGAAGATGTACTTTCATCAGCATGGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
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 QY 1441 CCGGACACACGCTTACCGATGGATCTTCTTGGGGAGATCTGCTGCTGCTGCTGCTGCTGCT 1500
 DB 1441 CCGGACACACGCTTACCGATGGATCTTCTTGGGGAGATCTGCTGCTGCTGCTGCTGCTGCT 1500
 QY 1501 CCGGCGCAGCAGCTGCTGCGGCTGACACCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
 DB 1501 CCGGCGCAGCAGCTGCTGCGGCTGACACCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
 QY 1561 CATTTCAATGCTGCTGCTGAGGAGTTCCTCATGATGCGCGGGCTTTGAGACTGCTGCTGCT 1620
 DB 1561 CATTTCAATGCTGCTGCTGAGGAGTTCCTCATGATGCGCGGGCTTTGAGACTGCTGCTGCT 1620
 QY 1621 ATGGATCGGCTGCTCGCATCGGCAAGAAATTCATATGTCAGCGGAAAGCTCCGAG 1680
 DB 1621 ATGGATCGGCTGCTCGCATCGGCAAGAAATTCATATGTCAGCGGAAAGCTCCGAG 1680
 QY 1681 CCAAGTCCAGCAGCAGTGGTGGCATCATGAGCAGACACTTGGTGGCAACATGACAGAGAC 1740
 DB 1681 CCAAGTCCAGCAGCAGTGGTGGCATCATGAGCAGACACTTGGTGGCAACATGACAGAGAC 1740
 QY 1741 ATGGCTCGGGGTGTTTCGGGCTCGGCGCCCGAGCAGAGCTCAGCTTGTGGAAGGCA 1800
 DB 1741 ATGGCTCGGGGTGTTTCGGGCTCGGCGCCCGAGCAGAGCTCAGCTTGTGGAAGGCA 1800
 QY 1801 GTACTGTGGAGCAGCTGTTACATGCGCCCTTCAGGCAGCTGCTGTGACCTCAATGTG 1860
 DB 1801 GTACTGTGGAGCAGCTGTTACATGCGCCCTTCAGGCAGCTGCTGTGACCTCAATGTG 1860
 QY 1861 GCGATGCGCTGACTCATCAGCGGGGCTCTGCGCTCTGCGCTGCTGCTGCTGCTGCTGCTG 1920
 DB 1861 GCGATGCGCTGACTCATCAGCGGGGCTCTGCGCTCTGCGCTGCTGCTGCTGCTGCTGCTG 1920
 QY 1921 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
 DB 1921 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
 QY 1981 CGAGCTGGCCCATGGGCATCCACCTCCCGCTGCGCCCGCCACCTGCGCCGAACTGCGAC 2040
 DB 1981 CGAGCTGGCCCATGGGCATCCACCTCCCGCTGCGCCCGCCACCTGCGCCGAACTGCGAC 2040
 QY 2041 GCGAGCTTATCCCGGGCAGGGGCTCCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
 DB 2041 GCGAGCTTATCCCGGGCAGGGGCTCCAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
 QY 2101 GGTGAGCGGGCTGAGGACCTCGGGGCGCGCCACTCTCAGCTCCCAACCTCTCTGCTGCT 2160
 DB 2101 GGTGAGCGGGCTGAGGACCTCGGGGCGCGCCACTCTCAGCTCCCAACCTCTCTGCTGCT 2160
 QY 2161 CAGCGGCAACAGCGCATGGCTCTCTGGGGCTAAGGGATCAGGAAGTGAAGGCTGCTGCT 2220
 DB 2161 CAGCGGCAACAGCGCATGGCTCTCTGGGGCTAAGGGATCAGGAAGTGAAGGCTGCTGCT 2220
 QY 2221 CCCTCAGGCTTCTGGGCAAACTCTCAAGGACAGCGCCAGCGCCCGCCAGGCAACAGTGCCT 2280
 DB 2221 CCCTCAGGCTTCTGGGCAAACTCTCAAGGACAGCGCCAGCGCCCGCCAGGCAACAGTGCCT 2280
 QY 2281 GAGCAGCGCAACACCGGGGCTCTCCAGCTTCTGCGCAACATGTAA 2325
 DB 2281 GAGCAGCGCAACACCGGGGCTCTCCAGCTTCTGCGCAACATGTAA 2325

PT identify hyperpolarization-activated cation channels modulators for treating familial sinus rhythm diseases, and ventricular arrhythmias.

The present sequence is the coding sequence for human hyperpolarisation activated channel 3 (HAC3). This protein comprises an alpha-subunit of a cation channel, which forms upon hyperpolarisation, a cation channel with an additional HAC. Modulators of HAC activity are useful for treating various pacemaker dysfunctions such as familial sinus rhythm diseases, sick sinus syndrome associated with atrial fibrillation, sinus tachycardias and bradycardias as well as ventricular arrhythmias. The modulators are also useful for treating other disorders involving abnormal ion flux, e.g., memory and learning disorders, sleeping disorders, bipolar disease, schizophrenia, central nervous system (CNS) disorders such as migraines, hearing and vision problems, seizures, and as neuroprotective agents (e.g. to prevent stroke). The Human HAC3 coding sequence is useful for treating the disorders by gene therapy.

Sequence 2325 BP; 411 A; 768 C; 675 G; 471 T; 0 U; 0 Other;

Query Match 100.0%; Score 2325; DB 3; Length 2325;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2325; Conservative 0; Mismatches 0; Indels 0;

	Qy	1	ATGGAGCAGACAGCGCCGCGGGGCCACGAAAGGBCGCACCCCTCGACTGAG	60
	Db	1	ATGGAGCAGACAGCGCCGCGGGGCCACGAAAGGBCGCACCCCTCGACTGAG	60
	Qy	61	GCGGTGCCTCCCGTTGCTCCCCCGCTCGCAACCGCGCCTCAGGTCCGATCCCACAATCT	120
	Db	61	GCGGTGCCTCCCGTTGCTCCCCCGCTCGCAACCGCGCCTCAGGTCCGATCCCANAATCT	120
	Qy	121	GGGCTTGAGCCTAAGAGAGGCACTTGGGACGCTGCTCAGCCTACGGTCAAAGAATTC	180
	Db	121	GGGCTTGAGCCTAAGAGAGGCACTTGGGACGCTGCTCAGCCTACGGTCAAAGAATTC	180
	Qy	181	TCCCTTCGGGTCTTCGGCAGGCACAAAACAGTGAATTCGAGCAGGAGCGGGTGAATCA	240
	Db	181	TCCCTTCGGGTCTTCGGCAGGCACAAAACAGTGAATTCGAGCAGGAGCGGGTGAATCA	240
	Qy	241	GGGGGGCCTTGATCATCAACCCCTACAGGACATTCCGGTTTTACTGGGACCTGATCATG	300
	Db	241	GGGGGGCCTTGATCATCAACCCCTACAGGACATTCCGGTTTTACTGGGACCTGATCATG	300
	Qy	301	CTGCTGCTGATGCTGGGAACTCATCGTCTGCTGTGGGCATCACCTTCTTCAAGGAG	360
	Db	301	CTGCTGCTGATGCTGGGAACTCATCGTCTGCTGTGGGCATCACCTTCTTCAAGGAG	360
	Qy	361	GAGAACTCCCGCCTTGGATCGTCTTCAACGTATTGTCTGATACTTTCTTCTTACTGGAT	420
	Db	361	GAGAACTCCCGCCTTGGATCGTCTTCAACGTATTGTCTGATACTTTCTTCTTACTGGAT	420
	Qy	421	CTGTGTCTCACTTCCGAACGGGATCGTGTGGAGGAGGCTCTGAGATCCCTGCTGGCA	480
	Db	421	CTGTGTCTCACTTCCGAACGGGATCGTGTGGAGGAGGCTCTGAGATCCCTGCTGGCA	480
	Qy	481	CCGCGGGCCATCCGACCGCTACTCTGCGCACATGTTTCTGTGTGACCTCATCTCTCT	540
	Db	481	CCGCGGGCCATCCGACCGCTACTCTGCGCACATGTTTCTGTGTGACCTCATCTCTCTCT	540
	Qy	541	ATCCCTGTGGATTACATCTTCTAGTGTGGAGCTGGAGCCAAGTTGANCCTGAGGTC	600
	Db	541	ATCCCTGTGGATTACATCTTCTAGTGTGGAGCTGGAGCCAAGTTGANCCTGAGGTC	600
	Qy	601	TACAAAAACGGCACGGGGCCTACGCATCGTTTCGCTTACCACCAAGATCCTAAGCCTGCTGAGG	660
	Db	601	TACAAAAACGGCACGGGGCCTACGCATCGTTTCGCTTACCACCAAGATCCTAAGCCTGCTGAGG	660
	Qy	661	CTGCTCCGCTCTCCCGCTCATTCGGTACATACACCAAGTGGAGAGATCTTTTACATG	720
	Db	661	CTGCTCCGCTCTCCCGCTCATTCGGTACATACACCAAGTGGAGAGATCTTTTACATG	720

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OM nucleic - nucleic search, using sw model

Run on: June 26, 2006, 22:18:28 ; Search time 1446 Seconds
(without alignments)
11210.565 Million cell updates/sec

Title: US-09-767-597-2
Perfect score: 2325
Sequence: 1 atggagcagacagcggcc.....agcttctgccaacatgtaa 2325

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqn1990s.*
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5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
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10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*
15: Geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2325	100.0	2325	3 AAC66779	AAC66779 Human hyp
2	2323.4	99.9	2325	8 ABZ75841	ABZ75841 Human HCN
3	2323.4	99.9	2325	8 ABZ58682	ABZ58682 Human HCN
4	2323.4	99.9	2325	8 ACA61916	ACA61916 cDNA enco
5	2323.4	99.9	2325	10 ABX95515	ABX95515 cDNA enco
6	2323.4	99.9	2325	14 AEB12299	AEB12299 Human HCN
7	2320.6	99.8	2340	6 ABK86387	ABK86387 Human HCN
8	2320.6	99.8	2340	6 ABK86386	ABK86386 Human HCN
9	2320.2	99.8	3852	6 AAL44691	AAL44691 Human tra
10	2319	99.7	2340	6 ABK86385	ABK86385 Human HCN
11	2215.4	95.3	3601	12 ADQ83229	ADQ83229 Human tum
12	2215.4	95.3	3601	13 ADQ85140	ADQ85140 Human tum
13	2122.6	91.3	2217	8 ABX71090	ABX71090 Novel hum
14	2115.4	91.0	3209	13 ACN43221	ACN43221 Human dia
15	2110.4	90.8	3496	6 AAD29758	AA29758 Human hyp
16	1910.4	82.2	3438	3 AAG62050	AAG62050 Hydropob
17	1876.2	80.7	2340	14 AEB12318	AEB12318 Mouse HCN
18	1872.8	80.6	2343	14 AEB12314	AEB12314 Rat HCN3

19	1810.4	77.9	1812	14 AEB12323	AEB12323 Human HCN
20	1721.8	74.1	3567	12 ADH22603	ADH22603 cDNA enco
21	1087.4	46.8	4751	2 AAZ09496	AAZ09496 Human hea
22	1085.8	46.7	4751	14 AEB12300	AEB12300 Human HCN
23	1085.8	46.7	4751	6 AAD29757	AA29757 Human hyp
24	1085.8	46.7	5065	4 AAH48730	AAH48730 Human HCN
25	1085.8	46.7	5065	13 ADR86593	ADR86593 Human HCN
26	1085.8	46.7	5499	4 ABA09197	ABA09197 Human cat
27	1073.2	46.2	3597	14 AEB12315	AEB12315 Rat HCN4
28	1061.6	45.7	2214	14 AEB12324	AEB12324 Human HCN
29	1061.6	45.7	2256	14 AEB12325	AEB12325 Human HCN
30	1054	45.3	3606	14 AEB12319	AEB12319 Mouse HCN
31	1045.4	45.0	3372	4 AAH48729	AAH48729 Human HCN
32	1045.4	45.0	3372	13 ADQ83419	ADQ83419 Human tum
33	1043.8	44.9	2670	14 AEB12298	AEB12298 Human HCN
34	1043.8	44.9	3459	6 AAD29756	AA29756 Human hyp
35	1043.4	44.9	2160	14 AEB12322	AEB12322 Human HCN
36	1019.2	43.8	2871	14 AEB12313	AEB12313 Rat HCN2
37	1016.2	43.7	1790	2 AAH84445	AAH84445 Human bra
38	1012.6	43.6	1820	2 AAZ09488	AAZ09488 Bovine re
39	1007.8	43.3	2886	2 AAZ09491	AAZ09491 Human Ih
40	1006.4	43.3	2592	14 AEB12317	AEB12317 Mouse HCN
41	1006.4	43.3	3102	4 AAH48731	AAH48731 Murine HC
42	983.8	42.3	2125	10 ADC87558	ADC87558 Human GPC
43	980.6	42.2	1584	2 AAH84444	AAH84444 Mouse bra
44	928.2	39.9	3431	4 AAH98302	AAH98302 Human EST
45	880	37.8	2817	14 AEB12321	AEB12321 Rainbow t

ALIGNMENTS

RESULT 1
AAC66779
ID AAC66779 standard; cDNA; 2325 BP.

XX AAC66779;

DT 16-FEB-2001 (first entry)

XX Human hyperpolarisation-activated channel HAC3 coding sequence.

XX Human; hyperpolarisation-activated channel; HAC3; neuroleptic; nontropic;
cerebroprotective; antigrains; antiarrhythmic; gene therapy;
pacemaker dysfunction; familial sinus rhythm disease;
sick sinus syndrome associated with atrial fibrillation;
sinus tachycardia; bradycardia; ventricular arrhythmia; bipolar disease;
schizophrenia; central nervous system disorder; migraine; seizure;
stroke; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 1..2325
FT /*tag= a
FT /product= "Human HAC3"

XX WO200063349-A1.

XX 26-OCT-2000.

XX 13-APR-2000; 2000NO-US009865.

XX 15-APR-1999; 99US-0129456P.

XX (ICAG-) ICAGEN INC.

XX Jegla TJ;

XX WPI; 2000-679592/66.

XX P-PSDB; AAB28375.

XX Novel human hyperpolarization activated channel 3 polypeptide useful to

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2006, 23:05:18 ; Search time 10971 Seconds
(without alignments)
11850.556 Million cell updates/sec

Title: US-09-767-597-2
Perfect score: 2325
Sequence: 1 atggaggcagagcggcc.....agctttctgccaacatgtaa 2325

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
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1: gb_est1.*
2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
5: gb_est6.*
6: gb_est7.*
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8: gb_est7.*
9: gb_est8.*
10: gb_est9.*
11: gb_gss1.*
12: gb_gss2.*
13: gb_gss3.*
14: gb_gss4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1876.2	80.7	3265	AK032225	Mus muscu
2	1803.6	77.6	4015	AK082719	Mus muscu
3	1619	69.6	1620	AY399924	Homo sapi
4	1315.8	56.6	1638	AY399926	Mus muscu
5	1292.2	55.6	1620	AY399925	Pan trogl
6	1045	44.9	1794	BC039619	Homo sapi
7	875.2	37.6	1725	DQ051256	Homo sapi
8	840.4	36.1	1689	DQ051257	Pan trogl
9	747.2	32.1	1087	BE798933	601583714
10	723.6	31.1	912	CD513082	AGNCOURT
11	716.2	30.8	858	BE793179	601581483
12	682.2	29.3	963	BE793179	602867826
13	673.6	29.0	815	CV675880	il48a08.k
14	667.4	28.7	692	BE7918260	603182933
15	637.4	27.0	771	DR000745	TC122071
16	607	26.1	780	BE260963	601151693
17	600.2	25.8	605	CV030457	9582 Full
18	594	25.5	810	DR762372	HSC4 139
19	587.4	25.3	776	CV107914	AGNCOURT

20	585	25.2	785	8	CN528592	CN528592	UT-M-HQ0-
21	582.4	25.0	1121	10	DM602851	DM602851	CGX162-E0
22	577.4	24.8	965	2	BI490063	BI490063	603031868
23	568.6	24.5	811	10	DV880381	DV880381	LB02613.C
24	565.4	24.3	567	9	DA169687	DA169687	DA169687
25	565.4	24.3	954	4	CB201579	CB201579	AGNCOURT
26	564.4	24.3	566	9	DA522053	DA522053	DA522053
27	563	24.2	565	9	DA770024	DA770024	DA770024
28	559.4	24.1	677	9	DR005083	DR005083	TC121938
29	557.4	24.0	559	9	DA811505	DA811505	DA811505
30	551.4	23.7	554	9	DA414799	DA414799	DA414799
31	546.4	23.5	548	9	DA626265	DA626265	DA626265
32	540	23.2	562	9	DA523993	DA523993	DA523993
33	539.2	23.2	728	3	BM944254	BM944254	UT-M-EHOP
34	536.8	23.1	635	9	DR003598	DR003598	TC122041
35	526.4	22.6	913	4	CA488537	CA488537	AGNCOURT
36	524.6	22.6	717	5	CK599046	CK599046	AGNCOURT
37	524	22.5	852	2	BI752028	BI752028	603022143
38	519.6	22.3	786	2	BG974320	BG974320	602844071
39	504	21.7	881	2	BG298718	BG298718	602396636
40	495.4	21.3	1030	3	BQ070889	BQ070889	AGNCOURT
41	494.4	21.3	496	9	DB169730	DB169730	DB169730
42	491	21.1	590	9	DA722534	DA722534	DA722534
43	484.2	20.8	800	10	DV882949	DV882949	LB02625.C
44	484	20.8	592	9	DA809823	DA809823	DA809823
45	480.4	20.7	895	4	CA488767	CA488767	AGNCOURT

ALIGNMENTS

RESULT 1	AK032225	3265 bp	mRNA	linear	HTC 02-SEP-2005
LOCUS	Mus musculus adult male olfactory brain cDNA, RIKEN full-length				
DEFINITION	enriched library, clone:6430507E23				
	product:hyperpolarization-activated, cyclic nucleotide-gated K+ 3,				
	full insert sequence.				
ACCESSION	AK032225				
VERSION	AK032225.1	GI:26328056			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;				
	Sciurognathi; Muridea; Muridae; Murinae; Mus.				
REFERENCE	1				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,				
	Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
	Normalization and subtraction of cap-trapper-selected cDNAs to				
	prepare full-length cDNA libraries for rapid discovery of new genes				
	Genome Res. 10 (10), 1617-1630 (2000)				
	11042159				
REFERENCE	3				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,				
	Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,				
	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,				
	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,				
	Fujitake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, R., Watahiki, M.,				
	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,				
	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
	RIKEN integrated sequence analysis (RISA) system--384-format				
	sequencing pipeline with 384 multicapillary sequencer				
	Genome Res. 10 (11), 1757-1771 (2000)				
	11076861				
	4				
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the				
JOURNAL	PANTOM Consortium.				
PUBMED					
REFERENCE					
AUTHORS					

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: June 26, 2006, 23:05:14 ; Search time 438 Seconds
(without alignments)
9932.256 Million cell updates/sec

Title: US-09-767-597-2

Perfect score: 2325

Sequence: 1 atggaggcagcagcgccgccc.....agctttctgccaacatgtaa 2325

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents/NA:

- 1: /EMC Celerera SIDS3/ptodata/2/ina/1 COMB.seq.*
- 2: /EMC Celerera SIDS3/ptodata/2/ina/5 COMB.seq.*
- 3: /EMC Celerera SIDS3/ptodata/2/ina/6A COMB.seq.*
- 4: /EMC Celerera SIDS3/ptodata/2/ina/6B COMB.seq.*
- 5: /EMC Celerera SIDS3/ptodata/2/ina/7 COMB.seq.*
- 6: /EMC Celerera SIDS3/ptodata/2/ina/H COMB.seq.*
- 7: /EMC Celerera SIDS3/ptodata/2/ina/PCTUS COMB.seq.*
- 8: /EMC Celerera SIDS3/ptodata/2/ina/PP COMB.seq.*
- 9: /EMC Celerera SIDS3/ptodata/2/ina/RE COMB.seq.*
- 10: /EMC Celerera SIDS3/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2122.6	91.3	2976	3	US-09-774-528-317
2	2122.6	91.3	2976	3	US-10-120-988-317
3	1085.8	46.7	4276	3	US-09-949-016-4900
4	1085.8	46.7	5065	3	US-09-949-016-744
5	1085.8	46.7	5065	4	US-10-067-457-4
6	1047	45.0	3235	3	US-09-949-016-1392
7	1045.4	45.0	3372	3	US-09-949-016-165
8	1038.2	44.7	1792	3	US-09-086-436-40
9	1038.2	44.7	1792	3	US-09-086-436-40
10	1016.2	43.7	1790	3	US-08-997-685A-11
11	1006.4	43.3	3102	4	US-10-067-457-6
12	983.8	42.3	1512	3	US-09-086-436-32
13	980.6	42.2	1584	3	US-08-997-685A-3
14	935.8	40.2	1518	3	US-09-086-436-34
15	871.2	37.5	1507	3	US-09-172-423-3
16	844.6	36.3	1307	3	US-08-997-685A-5
17	825.8	35.5	2733	3	US-08-997-685A-1
18	784.2	33.7	3224	3	US-09-774-528-238
19	784.2	33.7	3224	3	US-10-120-988-238
20	740.4	31.8	2246	3	US-09-086-436-38
21	740.4	31.8	2263	3	US-08-997-685A-9
22	328.6	14.1	1083	3	US-09-270-767-1038
23	328.6	14.1	1083	3	US-09-270-767-16320

c	24	314.8	13.5	13011	2	US-08-791-849A-14	Sequence 14, Appl
	25	265.4	11.4	31467	3	US-09-949-016-13134	Sequence 13134, A
	26	265.4	11.4	31868	3	US-09-949-016-11907	Sequence 11907, A
	27	259.4	11.2	50453	3	US-09-949-016-16642	Sequence 16642, A
	28	259.4	11.2	51242	3	US-09-949-016-12486	Sequence 12486, A
	29	176.4	7.6	601	3	US-09-949-016-32298	Sequence 32298, A
	30	176.4	7.6	601	3	US-09-949-016-173035	Sequence 173035, A
	31	166	7.1	15108	3	US-09-949-016-11786	Sequence 11786, A
	32	166	7.1	15108	3	US-09-949-016-17205	Sequence 17205, A
	33	163.6	7.0	601	3	US-09-949-016-21135	Sequence 21135, A
	34	163.6	7.0	601	3	US-09-949-016-47503	Sequence 47503, A
	35	163.2	7.0	601	3	US-09-949-016-21136	Sequence 21136, A
	36	163.2	7.0	601	3	US-09-949-016-47504	Sequence 47504, A
	37	134	5.8	1040	3	US-08-949-016-36	Sequence 36, Appl
	38	129.2	5.6	601	3	US-09-949-016-21121	Sequence 21121, A
	39	129.2	5.6	601	3	US-09-949-016-47489	Sequence 47489, A
	40	122	5.2	1060	3	US-08-997-685A-7	Sequence 7, Appl
	41	120.6	5.2	601	3	US-09-949-016-21142	Sequence 21142, A
	42	120.6	5.2	601	3	US-09-949-016-47510	Sequence 47510, A
	43	117.8	5.1	601	3	US-09-949-016-21134	Sequence 21134, A
	44	117.8	5.1	601	3	US-09-949-016-47502	Sequence 47502, A
	45	107.2	4.6	601	3	US-09-949-016-21141	Sequence 21141, A

ALIGNMENTS

RESULT 1
US-09-774-528-317
; Sequence 317, Application US/09774528
; Patent No. 6743619
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wehrman, Tom
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6743619el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802
; CURRENT APPLICATION NUMBER: US/09/774,528
; CURRENT FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 317
; LENGTH: 2976
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(2174)
US-09-774-528-317

Query Match 91.3%; Score 2122.6; DB 3; Length 2976;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2125; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 197 GCACCCACCAAGCAGTGGAAATCGACGAGCGGGTGAAGTCAGCGGGCCCTGGATCA 256
Db 46 GCGTCCCAAGCAGTGGAAATCGACGAGCGGGTGAAGTCAGCGGGCCCTGGATCA 105
Qy 257 TCACACCCCTACAGCAGCTTCGGGTTTTTACTGGGACCTGATCATCTGCTGCTGATGGTGG 316
Db 106 TCACACCCCTACAGCAGCTTCGGGTTTTTACTGGGACCTGATCATCTGCTGCTGATGGTGG 165

Qy	181	TCCCTTCGGGTGTTTCGGCAGCCACAAGAGTGGAAATCGAGCAGGAGCGGGTGAAGTCA	240
Db	181	TCCCTTCGGGTGTTTCGGCAGCCACAAGAGTGGAAATCGAGCAGGAGCGGGTGAAGTCA	240
Qy	241	GGGGGGGCTGGATCATCCACCCCTACAGCAGCTTCGGGTTTTACTGGGACCTGATCATG	300
Db	241	GGGGGGGCTGGATCATCCACCCCTACAGCAGCTTCGGGTTTTACTGGGACCTGATCATG	300
Qy	301	CTGCTGCTGATGGTGGGAAACCTCATCGTCTCTGCTGTGGGCATCACCTCTTCAAGGAG	360
Db	301	CTGCTGCTGATGGTGGGAAACCTCATCGTCTCTGCTGTGGGCATCACCTCTTCAAGGAG	360
Qy	361	GAGAACTCCCGCCTTGGATCGTCTTCAACGTATGTCTGATACTTTCTCCTACTGGAT	420
Db	361	GAGAACTCCCGCCTTGGATCGTCTTCAACGTATGTCTGATACTTTCTCCTACTGGAT	420
Qy	421	CTGGTGCTCAACTTCCGAAACGGGCATCGTGTGTGGAGGGGTGCTGAGATCCTCTGGCA	480
Db	421	CTGGTGCTCAACTTCCGAAACGGGCATCGTGTGTGGAGGGGTGCTGAGATCCTCTGGCA	480
Qy	481	CCGGGGGCATCCGCAACGCGCTACTCGCGCACATGGTTCCTGGTTGACCTCATCTCTTCT	540
Db	481	CCGGGGGCATCCGCAACGCGCTACTCGCGCACATGGTTCCTGGTTGACCTCATCTCTTCT	540
Qy	541	ATCCCTGTGGATTAACATCTTCTAGTGTGGAGCTGGAGCCACCGTTTGGACGTGAGGTC	600
Db	541	ATCCCTGTGGATTAACATCTTCTAGTGTGGAGCTGGAGCCACCGTTTGGACGTGAGGTC	600
Qy	601	TACAAACGGCACGGGCCCTAGCATTGTTCCGCTTACCAAGATCTCTAAGCCTGCTGAGG	660
Db	601	TACAAACGGCACGGGCCCTAGCATTGTTCCGCTTACCAAGATCTCTAAGCCTGCTGAGG	660
Qy	661	CTGCTCCGCTCTCCGCTCATCCGCTACATACACAGTGGGAGGAGATCTTTTCACATG	720
Db	661	CTGCTCCGCTCTCCGCTCATCCGCTACATACACAGTGGGAGGAGATCTTTTCACATG	720
Qy	721	ACCTATGACCTGGCCAGTGCTGTGGTTGCGCATCTTCAACCTCATTTGGGATGATCTGCTG	780
Db	721	ACCTATGACCTGGCCAGTGCTGTGGTTGCGCATCTTCAACCTCATTTGGGATGATCTGCTG	780
Qy	781	CTATGTCATGGGATGGTGCTGCGAGTTCTGTGTGCCATGCTGCHAGGACTTCCCTCCC	840
Db	781	CTATGTCATGGGATGGTGCTGCGAGTTCTGTGTGCCATGCTGCHAGGACTTCCCTCCC	840
Qy	841	GACTGCTGGGTCTCCATCAACCAATGGTGAACCACTCGTGGGCGCCACAGTATTTCCCAT	900
Db	841	GACTGCTGGGTCTCCATCAACCAATGGTGAACCACTCGTGGGCGCCACAGTATTTCCCAT	900
Qy	901	GCCCTGTTCAAGGCCATGAGCCACATGCTGTGCATTGGCTATGGGCAGCAGGACCTGTGA	960
Db	901	GCCCTGTTCAAGGCCATGAGCCACATGCTGTGCATTGGCTATGGGCAGCAGGACCTGTGA	960
Qy	961	GGCATGCCGACGCTGGCTCACATGCTCAGCATGATCGTAGGTGCCACATGCTAGGCC	1020
Db	961	GGCATGCCGACGCTGGCTCACATGCTCAGCATGATCGTAGGTGCCACATGCTAGGCC	1020
Qy	1021	ATGTTTCATCGGCCATGCCACGGCACTCATCCAGTCCCTGGACTCTTCCCGCGCTGAGTAC	1080
Db	1021	ATGTTTCATCGGCCATGCCACGGCACTCATCCAGTCCCTGGACTCTTCCCGCGCTGAGTAC	1080
Qy	1081	CAGGAGAAGTACAAGCAGGTGGACAGTACATGTCTTCCCAAGCTGCCAGCAGACAGC	1140
Db	1081	CAGGAGAAGTACAAGCAGGTGGACAGTACATGTCTTCCCAAGCTGCCAGCAGACAGC	1140
Qy	1141	CGGCAGCGCATCCAGAGTACTATGAGGACCGCTTACAGGGCAAGATGTTTCGATAGGAA	1200
Db	1141	CGGCAGCGCATCCAGAGTACTATGAGGACCGCTTACAGGGCAAGATGTTTCGATAGGAA	1200
Qy	1201	AGCATCTTGGCGAGCTGAGCGGACCGCTTCCGAGGAGATCATTAATCTTCACTGTGCG	1260
Db	1201	AGCATCTTGGCGAGCTGAGCGGACCGCTTCCGAGGAGATCATTAATCTTCACTGTGCG	1260
Qy	1261	GGCTGTGTGGCCACATGCGCGCTGTTTGCCCATGCTCCGACCCACGCTTCGTCAGTGTT	1320

Db	1261	GGCCTGTGTGGCCACATGCGCGCTGTTTGGCCATGCGCA	CCCCAGCTTCGTCAC	TGTCAGTT	1320
Qy	1321	CTCACCAAGCTGCGCTTTTGAAGTCTTCCAGCGGGGAGTCTCGTGTGTGGTAGGGCTCC			1380
Db	1321	CTCACCAAGCTGCGCTTTGAGGTCTTCCAGCGGGGAGTCTCGTGTGTGGTAGGGCTCC			1380
Qy	1381	GTGGGGAGGAGATGTATCTTCATCCAGCATGGGCTGCTCAGTGTGTGTGGCCCCGCGCGCC			1440
Db	1381	GTGGGGAGGAGATGTATCTTCATCCAGCATGGGCTGCTCAGTGTGTGTGGCCCCGCGCGCC			1440
Qy	1441	CGGAGACACGCTCACCGATGATCTTCTTTGGGGAGATCTGCTCTCTAACTAGGGGC			1500
Db	1441	CGGAGACACGCTCACCGATGATCTTCTTTGGGGAGATCTGCTCTCTAACTAGGGGC			1500
Qy	1501	CGGCGCACAGCAGTGTTCGGGCTGACACACTACTGCGCGCTTTTACTCACTCAGCGTGGAC			1560
Db	1501	CGGCGCACAGCAGTGTTCGGGCTGACACACTACTGCGCGCTTTTACTCACTCAGCGTGGAC			1560
Qy	1561	CATTTCATGCTGTGCTTGAGGAGTTCCTCCATGATGCGCGGCGCTTTGAGACTGTGGCC			1620
Db	1561	CATTTCATGCTGTGCTTGAGGAGTTCCTCCATGATGCGCGGCGCTTTGAGACTGTGGCC			1620
Qy	1621	ATGATCGGCTGTCCGCATCGGCAAGAGAAATTCATCTGACGCGGAAGCGCTCCGAG			1680
Db	1621	ATGATCGGCTGTCCGCATCGGCAAGAGAAATTCATCTGACGCGGAAGCGCTCCGAG			1680
Qy	1681	CCAAGTCCAGGCAGCAGTGTGTGCATCATGAGCAGCAGCTTGTGTGCAACATGACACAGAC			1740
Db	1681	CCAAGTCCAGGCAGCAGTGTGTGCATCATGAGCAGCAGCTTGTGTGCAACATGACACAGAC			1740
Qy	1741	ATGCTCTCGGGGTGTTTCGGGGTCGGGGCCCCGAGCACAGGAGCTCAGCTTGTGTGAAAGCCA			1800
Db	1741	ATGCTCTCGGGGTGTTTCGGGGTCGGGGCCCCGAGCACAGGAGCTCAGCTTGTGTGAAAGCCA			1800
Qy	1801	GTACTGTGGAGCAGCTGTGTACATGATGGCCCCCTTCAGGCAGCTGCTGTGACCTCCAATGTG			1860
Db	1801	GTACTGTGGAGCAGCTGTGTACATGATGGCCCCCTTCAGGCAGCTGCTGTGACCTCCAATGTG			1860
Qy	1861	GCCATTGCCCTGACTCATCAGCGGGGCGCTCTGCCCTCTCCCTCAGCTCTCCAGCCACC			1920
Db	1861	GCCATTGCCCTGACTCATCAGCGGGGCGCTCTGCCCTCTCCCTCAGCTCTCCAGCCACC			1920
Qy	1921	CTCTTGTCTCGTCTGTGTGGGCTCAGCAGGCTCTCCAGCTTCCCCTGTGTGCCCCGT			1980
Db	1921	CTCTTGTCTCGCTGTGTGGGCTCAGCAGGCTCTCCAGCTTCCCCTGTGTGCCCCGT			1980
Qy	1981	CGAGCTGGCCCATGGGCATCCACTCCGCTGCGCGCCCCACCTGCGCGAACCTTCGAC			2040
Db	1981	CGAGCTGGCCCATGGGCATCCACTCCGCTGCGCGCCCCACCTGCGCGAACCTTCGAC			2040
Qy	2041	GCCAGCCTATCCGGGACAGGCGCTCCAGGCTCTCCCTGTGTGGTCCCCCTCCAGGAGGA			2100
Db	2041	GCCAGCCTATCCGGGACAGGCGCTCCAGGCTCTCCCTGTGTGGTCCCCCTCCAGGAGGA			2100
Qy	2101	GGTGGACGGCGGTAGAGACCTCGGGGCGGCCACTCTCAGCTTCCCAACCTCTCTGCGCT			2160
Db	2101	GGTGGACGGCGGTAGAGACCTCGGGGCGGCCACTCTCAGCTTCCCAACCTCTCTGCGCT			2160
Qy	2161	CAGCGGCAACAGCGCATGCTCTCTGCGGCTAAGGGATCAGGAAGTGTAGCGGCTGCT			2220
Db	2161	CAGCGGCAACAGCGCATGCTCTCTGCGGCTAAGGGATCAGGAAGTGTAGCGGCTGCT			2220
Qy	2221	CCCTCAGGGCTCTGTGCCAAACCTCCAAAGACAGCCCCAGCCCCCAGGACACAGTGCCT			2280
Db	2221	CCCTCAGGGCTCTGTGCCAAACCTCCAAAGACAGCCCCAGCCCCCAGGACACAGTGCCT			2280
Qy	2281	GAGCGACACACCCCGGGGTCTCCAGCTTTCTGTGCCAAATGTAA			2325
Db	2281	GAGCGACACACCCCGGGGTCTCCAGCTTTCTGTGCCAAATGTAA			2325

RESULT 2

1098 GGTGGAGCAGTACATGCTCTTCCACAAAGCTGCCAGCAGACACGCGGCGGCGATCCACGA 1157
 1424 CTCGGAGCAGTGGATGATCACCACCGCTCTCTCCCCAGGAGCTCCGGGAGGCGTCCGCG 1483
 1158 GTACTATGACCCGGT---ACAGGGCAAGATGTTCCGATGAGGAAAGCATCTGGGCGA 1214
 1484 CTACGACGCTTACAAGTGGGTCAACACCGCGGCGTCCGACGAGGAGTCTCTGTCGCCAA 1543
 1215 GCTGAGGAGCCGCTTCGGGAGGAGATCATTAATCTTCACTGTCGGGGCTGGTGCCCA 1274
 1544 CTTCCCAAGGACCTCCGCGCGACATCAAGCCCACTCTGCTCGGCTCTGTCGCGCG 1603
 1275 CATGCGCTGTTTGGCCATGCGCCAGCCCACTTCTGCTCACTGCTGCTCACTCAACAAAGCTGG 1334
 1604 CGTCCGCTCTTCCGCAACATGACGAGCGCTCTCTCGACGCACTCTGCGAGCGCTCCG 1663
 1335 CTTTGAAGTCTTCCAGCGGGGATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1394
 1664 CCGCGGCTCTACACGAGCGCACTTCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 1723
 1395 GTACTTCATCCAGCAGTGGCTGCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1454
 1724 GCTCTTCATATCCGCGGCTGCTCGAGAGCATCAACCGAGCGGCGGCGGCTTCCGGCTT 1783
 1455 CACCGATGATCTTCTTGGGAGATCTGCCT 1487
 1784 CTTCAACCGCAGCTCTCTCGAGGAGCGACTT 1816

RESULT 2

US-11-302-678-27
 ; Sequence 27, Application US/11302678
 ; Publication No. US2006008881A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Silos-Santiago, Immaculada
 ; APPLICANT: Venkateswarlu, Karicheti
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
 ; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
 ; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46556, 62553, 302, 323,
 ; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
 ; FILE REFERENCE: MPI02-012PIRNM OMNI
 ; CURRENT APPLICATION NUMBER: US/11/302,678
 ; CURRENT FILING DATE: 2005-12-14
 ; PRIOR APPLICATION NUMBER: US/10/345,680
 ; PRIOR FILING DATE: 2003-01-16
 ; PRIOR APPLICATION NUMBER: US 60/349,511
 ; PRIOR FILING DATE: 2002-01-18
 ; PRIOR APPLICATION NUMBER: US 60/360,500
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/365,041
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 60/374,063
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/403,468
 ; PRIOR FILING DATE: 2002-08-14
 ; PRIOR APPLICATION NUMBER: US 60/414,262
 ; PRIOR FILING DATE: 2002-09-27
 ; PRIOR APPLICATION NUMBER: US 60/419,986
 ; PRIOR FILING DATE: 2002-10-21
 ; PRIOR APPLICATION NUMBER: US 60/423,809
 ; PRIOR FILING DATE: 2002-11-05
 ; PRIOR APPLICATION NUMBER: US 60/429,797
 ; PRIOR FILING DATE: 2002-11-26
 ; NUMBER OF SEQ ID NOS: 66
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 2085
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(2085)

US-11-302-678-27
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 Best Local Similarity 47.8%; Pred. No. 1.7e-06;
 Matches 266; Conservative 0; Mismatches 281; Indels 9; Gaps 2;
 QY 993 CATGATCGTAGTGCCACATGCTACGCCATGTTTCATCGGCCATCCAGCGGCACTCATCCA 1052
 DB 1152 CTTCTTGGTGGTGTCTGATTTTGGCCACCATGTTGGGCAATGTTGGGCTCCATGATCTC 1211
 QY 1053 GTCCCTGAGCTCTTCCCGGCGTCACTACGAGGAGAAAGTACAAGCAGGTGGAGAGTACAT 1112
 DB 1212 GAATATGAATCCCTACCGGCGAGAGTTCCAGGCCAAGATTGATTCATCAAGCAGTACAT 1271
 QY 1113 GTCCCTCCACAAGCTGCCAGCAGACACGCGCAGCGATCCACGAGTACTATGAGCACGG 1172
 DB 1272 GAGTTCGCAAGGTCCAAAGGACTTGGAGACCGGGTTATCCGGTGGTTGACTACTCT 1331
 QY 1173 CTA---CCAGGGCAAGATGTTTCGATGAGGAAAGCATCTCGGGCGAGCTGAGCGAGCGCT 1229
 DB 1332 GTGGGCCAACAAGAGACGGTGGATGAGAGGAGGTGCTCAAGAGCCTCCCGACAAAGCT 1391
 QY 1230 TCGCAGAGAGATCAATTAATCTTCACTGTGCGGGGCTGTGTCGCCACATGCGCGCTGTTGC 1289
 DB 1392 GAAGGCTGAGATCGCCATCAACGTGCACCTGGACACGCTGAAGAAGGTTCGCATCTTCCA 1451
 QY 1290 CCATCGCGACCCAGCTTCGTCACTGCGAGTTCTCACCAGCTGCGCTTTGAGGTCTTCCA 1349
 DB 1452 GGACTGTGAGGACGGCTGCTGGTGGAGCTGGTGAAGCTGCGACCCACTGTGTTGAG 1511
 QY 1350 CCGCGGGGATCTCGTGTGTCGTGAGGGTCCGTGGGAGGAGATGTACTTTCATCCAGCA 1409
 DB 1512 CCCTGGGATATATCTCAAGAGGAGAGATATTTGGGAGGAGATGTATCATCATCAACGA 1571
 QY 1410 TGGGCTGCTCAGTGTGCTGGC-----CCGCGGCGCCGCGGACACACGCCCTCACCGATGG 1463
 DB 1572 GGGCAAGCTGGCGCTGTGCTGATGATGCGGTCAACCCAGTTCTGTTGCTCTCAGCGATGG 1631
 QY 1464 ATCTACTTTGGGAGATCTGCTTAACTAGGGGCGCGGCGACAGCCAGTGTTCGGGC 1523
 DB 1632 CAGTACTTTCGGGAGATCAGCATTTGAAACATCAAGGGGAGCAAGTGGGGAACCGAG 1691
 QY 1524 TGACACCTTACTGCGCGC 1539
 DB 1692 GACGCCCAACATCCGC 1707

RESULT 3

US-11-302-678-25
 ; Sequence 25, Application US/11302678
 ; Publication No. US2006008881A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Silos-Santiago, Immaculada
 ; APPLICANT: Venkateswarlu, Karicheti
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
 ; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
 ; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46556, 62553, 302, 323,
 ; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
 ; FILE REFERENCE: MPI02-012PIRNM OMNI
 ; CURRENT APPLICATION NUMBER: US/11/302,678
 ; CURRENT FILING DATE: 2005-12-14
 ; PRIOR APPLICATION NUMBER: US/10/345,680
 ; PRIOR FILING DATE: 2003-01-16
 ; PRIOR APPLICATION NUMBER: US 60/349,511
 ; PRIOR FILING DATE: 2002-01-18
 ; PRIOR APPLICATION NUMBER: US 60/360,500
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/365,041
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 60/374,063
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/403,468

GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM nucleic - nucleic search, using sw model
 Run on: June 26, 2006, 23:15:26 ; Search time 90 Seconds
 (without alignments)
 6192.891 Million cell updates/sec
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 Perfect score: 2325
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 Scoring table: IDENTITY NUC
 Gapop 10.0 , Gapext 1.0
 Searched: 296510 seqs, 119862409 residues
 Total number of hits satisfying chosen parameters: 593020

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries
 Database : Published Applications NA New.*
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 2: /EMC_Celerra_SID33/ptodata/2/pubpna/US06_NEW_PUB.seq.*
 3: /EMC_Celerra_SID33/ptodata/2/pubpna/US07_NEW_PUB.seq.*
 4: /EMC_Celerra_SID33/ptodata/2/pubpna/US08_NEW_PUB.seq.*
 5: /EMC_Celerra_SID33/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
 6: /EMC_Celerra_SID33/ptodata/2/pubpna/US10_NEW_PUB.seq.*
 7: /EMC_Celerra_SID33/ptodata/2/pubpna/US11_NEW_PUB.seq.*
 8: /EMC_Celerra_SID33/ptodata/2/pubpna/US60_NEW_PUB.seq.*
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77.8	3.3	2544	US-10-449-902-18848	Sequence 18848, A
2	68.4	2.9	2085	US-11-302-678-27	Sequence 27, Appl
3	68.4	2.9	3486	US-11-302-678-25	Sequence 25, Appl
4	57.2	2.5	3083	US-11-312-958-29	Sequence 29, Appl
5	56.4	2.4	2326	US-10-449-902-17165	Sequence 17165, A
6	55.8	2.4	1580	US-10-449-902-2520	Sequence 2520, Ap
7	48.8	2.1	2439	US-10-449-902-25641	Sequence 25641, A
8	48.4	2.1	152331	US-11-175-714-86	Sequence 86, Appl
9	48.2	2.1	1320	US-10-449-902-19536	Sequence 19536, A
10	48	2.1	2064	US-10-449-902-9081	Sequence 9081, Ap
11	45.8	2.0	17203	US-10-517-441-121	Sequence 121, App
12	45.6	2.0	1222	US-10-449-902-25996	Sequence 25996, A
13	44.2	1.9	128361	US-10-505-928-151	Sequence 151, App
14	44.2	1.9	1184	US-10-449-902-11798	Sequence 11798, A
15	44.2	1.9	2745	US-10-449-902-20146	Sequence 20146, A
16	44.2	1.9	3553	US-11-312-958-17	Sequence 17, Appl
17	44	1.9	1304	US-10-449-902-28022	Sequence 28022, A
18	43.8	1.9	2410	US-10-449-902-24550	Sequence 24550, A
19	43.6	1.9	1679	US-10-449-902-10109	Sequence 10109, A
20	43	1.8	11978	US-11-257-851A-63	Sequence 63, Appl
21	42.8	1.8	4001	US-10-517-441-132	Sequence 132, App
22	42.8	1.8	84428	US-11-330-363-1	Sequence 1, Appl
23	42.6	1.8	1787	US-10-449-902-25521	Sequence 25521, A
24	42.2	1.8	580	US-10-953-349-27203	Sequence 27203, A
25	42.2	1.8	1441	US-10-953-349-28919	Sequence 28919, A

26	42	1.8	2092	6	US-10-449-902-19116	Sequence 19116, A
27	41.6	1.8	1480	6	US-10-449-902-16130	Sequence 16130, A
28	40.8	1.8	1123	6	US-10-449-902-23368	Sequence 23368, A
29	40.8	1.8	1256	6	US-10-449-902-8986	Sequence 8986, Ap
30	40.6	1.7	3580	7	US-11-289-102-32	Sequence 32, Appl
31	40.4	1.7	1986	6	US-10-449-902-6333	Sequence 6333, Ap
32	40.2	1.7	1317	6	US-10-449-902-24565	Sequence 24565, A
33	40.2	1.7	2796	6	US-10-449-902-19530	Sequence 19530, A
34	40	1.7	955	6	US-10-953-349-23686	Sequence 23686, A
35	40	1.7	1419	6	US-10-449-902-10331	Sequence 10331, A
36	40	1.7	1559	6	US-10-449-902-22528	Sequence 22528, A
37	40	1.7	1590	6	US-10-449-902-1559	Sequence 1559, Ap
38	40	1.7	1598	6	US-10-449-902-8452	Sequence 8452, Ap
39	40	1.7	1704	6	US-10-449-902-17171	Sequence 17171, A
40	40	1.7	2173	6	US-10-449-902-22156	Sequence 22156, A
41	40	1.7	2266	6	US-10-449-902-20171	Sequence 20171, A
42	40	1.7	2798	6	US-10-449-902-26902	Sequence 26902, A
43	39.8	1.7	1291	6	US-10-449-902-6445	Sequence 6445, Ap
44	39.6	1.7	1533	6	US-10-449-902-2853	Sequence 2853, Ap
45	39.6	1.7	2057	6	US-10-449-902-17942	Sequence 17942, A

ALIGNMENTS

RESULT 1
 US-10-449-902-18848
 ; Sequence 18848, Application US/10449902
 ; Publication NO. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agrobiological Sciences
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A0205V1-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 18848
 ; LENGTH: 2544
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: AK069229
 ; DATABASE ENTRY DATE: 2001-12-06
 US-10-449-902-18848

Query Match	3.3%	Score 77.8	DB 6	Length 2544
Best Local Similarity	46.3%	Pred. No. 1.5e-08		
Matches 293	Conservative 0	Mismatches 337	Indels 3	Gaps 1
QY	858	CAACACATGGTGAACCACTCGTGGGGCCGAGTATTCCTCCATGCCCTGTTCAAGGCCAT	917	
Db	1184	CGAGTCATCAAGTCAACGACTTCACCTCAAGTCTCTACTGCTCTGTTGGGGCT	1243	
QY	918	GAGCCACATGCTGTGCATTTGGCTATGGCAGCAGGCACCTGTAGGCATCCCGACGCTG	977	
Db	1244	TGCCAACCTCAGCACGCTGGGCAAGGGCTGCAGCAGCATATACACGGGGAGCGCT	1303	
QY	978	GTCACCATGCTCAGCATGATCGTAGGTGCCACATGCTACGCCATGTTTCATGGCCATGC	1037	
Db	1304	GTTCGATATTCCTGGGACGCTTCGGGCTGATCTCTGATGGCGATGCTGATCGGAACAT	1363	
QY	1038	CACGGCACTCATCCAGTCCCTGACTTCTCCCGGGGTGCTAGTACCAGGAGACTACAAGCA	1097	
Db	1364	CCAGACGTACCTGCAGTCATGACCGTGGAGGATGCGGGTGNACGGGGCGA	1423	

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OM protein - protein search, using sw model

Run on: June 26, 2006, 20:17:52 ; Search time 201 Seconds
(without alignments)
1760.624 Million cell updates/sec

Title: US-09-767-597-1
Perfect score: 4038
Sequence: 1 MEABQRPACASGATPGLE.....PRPPVPEPATPRGLQLSANM 774

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues
Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : A Geneseq 8.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*
- 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4038	100.0	774	3	AAB28375 Human hyp
2	4038	100.0	774	5	AAO14208 Human tri
3	4038	100.0	774	6	ABU09681 Human HCN
4	4038	100.0	774	6	ABP71446 Human HCN
5	4038	100.0	774	6	ABP71038 Human HCN
6	4038	100.0	774	6	ABU10228 Human HCN
7	4028	99.8	774	6	AAU99980 Human HCN
8	4026	99.7	774	5	AAU99979 Human HCN
9	4022	99.6	774	5	AAU99978 Human HCN
10	3837.5	95.0	741	8	ABM84569 Human dia
11	3670	90.9	703	5	AAE18678 Human hyp
12	2540	62.9	1203	4	AAAB86462 Human HCN
13	2540	62.9	1203	5	AAE18677 Human hyp
14	2540	62.9	1203	8	ADR86636 Human HCN
15	2540	62.9	1245	4	ABE11953 Human cat
16	2402	59.5	889	4	AAAB86461 Human HCN
17	2402	59.5	889	4	AAE18676 Human hyp
18	2402	59.5	889	9	AAE17266 Human cyc
19	2391.5	59.2	863	4	AAAB86463 Murine HCN
20	2350	58.2	882	5	AAE21167 Human TRI
21	2346	58.1	882	8	ADR44920 Polypepti
22	2346	58.1	890	5	AAU11712 Human HCN
23	2346	58.1	890	6	ABU09680 Human HCN

24	2346	58.1	890	6	ABP71445 Human HCN
25	2346	58.1	890	6	ABP71037 Human HCN
26	2346	58.1	890	6	ABU10227 Human HCN
27	2346	58.1	890	7	ADJ95124 Novel NOV
28	2345	58.1	837	5	ABJ10804 Rabbit HC
29	2344	58.0	890	5	ABJ10800 Human HCN
30	2341	58.0	890	5	ABJ10797 Human HCN
31	2341	58.0	890	5	AAU11714 Human ful
32	2340	57.9	890	5	ABJ10799 Human HCN
33	2340	57.9	890	5	ABJ10801 Human HCN
34	2340	57.9	890	5	ABJ10793 Human HCN
35	2333	57.8	890	5	ABJ10798 Human HCN
36	2333	57.8	890	5	ABJ10796 Human HCN
37	2332	57.8	890	5	ABJ10794 Human HCN
38	2329	57.7	890	5	ABJ10795 Human HCN
39	2325.5	57.6	827	5	AAU11711 Human HCN
40	2321.5	57.5	827	5	AAU11713 Human ful
41	2317	57.4	910	2	ABJ10802 Mouse bra
42	2316	57.4	910	2	AAV22191 Rat HCN1
43	2316	57.4	910	5	ABJ10803 Rat HCN1
44	2314	57.3	890	5	AAE18675 Human hyp
45	2298	56.9	898	5	ABJ10805 Consensus

ALIGNMENTS

RESULT 1
AAB28375
ID AAB28375 standard; protein; 774 AA.
XX
AC AAB28375;
XX
DT 16-FEB-2001 (first entry)
XX
DE Human hyperpolarisation-activated channel HAC3.
XX

XX Human; hyperpolarisation-activated channel; HAC3; neuroleptic; nootropic;
KW cerebroprotective; antimigraine; antiarrhythmic; gene therapy;
KW pacemaker dysfunction; familial sinus rhythm disease;
KW sick sinus syndrome associated with atrial fibrillation;
KW sinus tachycardia; bradycardia; ventricular arrhythmia; bipolar disease;
KW schizophrenia; central nervous system disorder; migraine; seizure;
KW stroke.
XX Homo sapiens.
XX WO200063349-A1.
XX
PD 26-OCT-2000.
XX
PF 13-APR-2000; 2000WO-US009865.
XX
PR 15-APR-1999; 99US-0129456P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ;
XX
DR WPI; 2000-679592/66.
XX
N-PSDB; AAC66779.
XX
PT Novel human hyperpolarization activated channel 3 polypeptide useful to
PT identify hyperpolarization-activated cation channels modulators for
PT treating familial sinus rhythm diseases, and ventricular arrhythmias.
XX
PS Claim 13; Page 78; 81pp; English.
XX
CC The present sequence is human hyperpolarisation activated channel 3
CC (HAC3). This protein comprises an alpha-subunit of a cation channel,
CC which forms upon hyperpolarisation, a cation channel with an additional
CC HAC. Modulators of HAC activity are useful for treating various pacemaker
CC dysfunctions such as familial sinus rhythm diseases, sick sinus syndrome

QY 407 SEPLREEIINFTCKGLVAHMLPAHADPSFTAVLTKLREVEVQPGDLVVRGSGVRKMY 466
Db 721 PECLOADI CILHNSRLLQHKCPFRGATYGCRLALAMKFKTHAPPDGLVHAGDILLTALY 780
QY 467 FIOHGLSVLARGARDRLTLDGSYFGE-ICLLTR-GRRTASVRADTYCRLYSLSVDHFA 524
Db 781 FISRGSTEILRGDVAAILKNDIFGEPLNLYARPGKNGSDVRALTYCDLKHHRDDLLE 840
QY 525 VLEEFPMRAFAFETVAMDRLLRIGKNSILQKRSEPPSS--GGIMEQH--LV 575
Db 841 VLDMPFSDHFW-SLEITFNLRDNTMI-----PGSPGSTELEGFSRQRKLSFR 893
QY 576 QHORD-----MARGVGRAPSTGAQLSGKPLVWELVHAPLOAAVTSNVALATH 626
Db 894 RTDKDTEQGEVAGLGRAGAPSS-----RGRP-----923
QY 627 QRGLPLSPDSPATLLARSAMRSAGSPASPLVVRAGPMWASTSRLPAPPARTLHASLSRA 686
Db 924 -GGPWGESPPSSPESSEDEGPRSSPL---RLVPSS---PRPP-----964
QY 687 GRSQVLLGPPPG-----GGRRLGPRGRPLSASQPSLPORAT--GDGSPGRKSGSERL 739
Db 965 -----GEPGGEPLMEDCEKSSDCTNPLSGAFSGVSNIFSFWGD-SRGROYQLPRC 1015
QY 740 P-PSGLLAKPRTAQP RP 757
Db 1016 PAPTPLLNLPLSSPGRRP 1034

RESULT 2
T31354
probable potassium channel elk chain 1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31354
R;Engelund, B.; Neu, A.; Ludwig, J.; Roeper, J.; Pongs, O.
submitted to the EMBL Data Library, July 1998
A;Description: Identification of three rat potassium channel genes homologous to D. melanogaster
A;Reference number: Z20983
A;Accession: T31354
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1017 <ENG>
A;Cross-references: UNIPROT:Q9R179; UNIPARC:UPI0000170A85; EMBL:AJ007628; NID:e13229997;
A;Experimental source: cortex
C;Genetics:
A;Gene: elk1
C;Keywords: potassium channel

Query Match 12.6%; Score 509; DB 2; Length 1017;
Best Local Similarity 25.3%; Pred. No. 1.7e-24;
Matches 204; Conservative 118; Mismatches 303; Indels 180; Gaps 29;

QY 46 RRLHGLTLOPTVKNKSLRVFGSHKA-----VEIEQERVKSGA---AWIHPYSDRRF 94
Db 170 RQRNRTVLRLHGLTGFGRDGGSVKANSVPEPKSPYEVKVASVGSGRCLLLH-YISPKA 228

QY 95 YNDLIMLLMVGNLVLPVGIITPFKEKNSP-----PMIVFNVLSDTFFLLDLVLFRTGIV 150
Db 229 VMDGLILLATFYVAVTVPVYVNCVAGDDTPIITSRHLTVSDIAVEMFLDILILNFTTV 288

QY 151 VEGABILLAPAIRTRYRTWFLVDLISIPVD--YIFLVLEPRPLDAEVYKTARALR 208
Db 289 SOSG-QVSGAPRSIGLHYLATWFFVDLIAALPFDLLYVFNIT-----329

QY 209 IVRFTKILSLRLRLIRLYHOWEIFHTMYDLASAVRIFNLIGHMMLLCHWDGCL 268
Db 330 ----VTSVLHLLKTVRLRLRLQLKLER-----YSQSAVV-LTLNLSVALLAHMMAVC 380

QY 269 QFLV-----PMLQDFPPDCWVSINHMVNSWGRQ-----YSHA 301
Db 381 WYVIGRREANDPLLDIG--WL-----HELKRLKEEPYVNSAGSPRSAYIAA 430

QY 302 LFKAMSHMLCIGYGQOAPVGMHPDVLTMLSMIVGATCYAMFIGHATALIQSLDSSRROY 361
Db 431 LYFTUSSSTVSGFNVNCANTDAEKIFSCTMLGMLHMAVFGVNTAIQRYSRSLYH 490
QY 362 EKYKQVEQYMFPHKLPAADTRQRIHEYYEHRYQ-GRMPDEESILGELSPLBEEIINFCTR 420
Db 491 SRMKDLKQFIRVHRLPRPLKQRMLEFYQTTWAVNSGIDANELLRPDPDELADIAMHLNR 550
QY 421 GLVAMPLFAHADPSFTAVLTKLREVEVQPGDLVVRGSGVRKMYFTQHGLLSVLAR-- 478
Db 551 ETL-QLPLFGAASRGCLRALSLIHKTSFCAPGEFLRRGDALQAHYYVCSSGLEVRDNT 609
QY 479 -----GARDTRLTDGYSFGEICLLTGRGTASVRADTYCRLYSLSVDHFNALVE 527
Db 610 VLAIGKGDILGADIPELQBPFGAGCVL---KTSADVKAITYCGLQQLSSRGIAELVLR 666
QY 528 EPPMRRRAFETVAMDRL---LRIGKNSILQKRSEP-----SPGSSGGIMEQHLYQ 576
Db 667 LYPEVVAFAFRAGLPRDLTFNLRQSENNGLGRFSRPLSQARSDTLSSSSDKTLPSITE 726
QY 577 HDRDMARGVRGRAPSTGAQLSGKPLVWELVHAPLOAAVTSNVAIALTHQRGLPLSPD 636
Db 727 TE-----GMEPEGAGS---KP-----RRPLLPLNL 748
QY 637 SPATLLARSAMRSAGSPASPL---VPVRAGPMWASTSRLPAPPARTLHASLSRAGR-SQVS 692
Db 749 SPA-----RPRGSLVSLIGEELPFPSALVSSPSLSTP-----SPALAGSGSSPS 793
QY 693 LLGPPPPGGRRRLGPRGRPLSASQPSLPORATGDSP-----GRKGGSGERLPPSGLLAKP 748
Db 794 LHGPPRGSA-----WKPQLLTPPLTGFPPDLSPWIVDIEDSSNTAEAPTRFRSKR 847
QY 749 PR-TAQP RP RP VPPEPATRGLQLSA 772
Db 848 PEPTRTSQAPLSGPRLSRELATEA 872

RESULT 3
A55251
cyclic nucleotide-gated Ca++ channel protein CNG-3 - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
C;Accession: A55251; S43976
R;Biel, M.; Zong, X.; Distler, M.; Bosse, E.; Klugbauer, N.; Murakami, M.; Flockert, V.
Proc. Natl. Acad. Sci. U.S.A. 91, 3505-3509, 1994
A;Title: Another member of the cyclic nucleotide-gated channel family, expressed in testis
A;Reference number: A55251; MUID:94224768; PMID:8170936
A;Accession: A55251
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-706 <BI>
A;Cross-references: UNIPROT:Q29441; UNIPARC:UPI0000127C20; GB:X76485; NID:g488728; PIDN
A;Experimental source: kidney
R;Weyand, I.; Godde, M.; Frings, S.; Weiner, J.; Mueller, F.; Altenhofen, W.; Hatt, H.;
Nature 368, 859-863, 1994
A;Title: Cloning and functional expression of a cyclic-nucleotide-gated channel from man
A;Reference number: S43976; MUID:94211295; PMID:7512693
A;Accession: S43976
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-706 <WE>
A;Cross-references: UNIPARC:UPI0000127C20; GB:X89600; NID:g908823; PIDN:CAA61759.1; PID
A;Experimental source: testis
C;Genetics:
A;Gene: CNG3
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide
C;Keywords: GMP binding; ion channel; ion transport; membrane protein
F:501-625/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 12.1%; Score 487.5; DB 2; Length 706;
Best Local Similarity 26.1%; Pred. No. 2.4e-23;
Matches 132; Conservative 115; Mismatches 215; Indels 43; Gaps 13;

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 26, 2006, 20:18:22 ; Search time 46 Seconds
(without alignments)
1618.952 Million cell updates/sec

Title: US-09-767-597-1
Perfect score: 4038
Sequence: 1 MEAEQRPACASSGATPGLE.....PRPVPEPATRGQLSANM 774

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Lifelong first 45 summaries

Database : PIR 80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	512.5	12.7	1159	2	probable potassium
2	509	12.6	1017	2	probable potassium
3	487.5	12.1	706	2	cyclic nucleotide-
4	485	12.0	695	2	cyclic nucleotide-
5	483.5	12.0	735	2	alpha subunit of c
6	483	12.0	664	2	cyclic nucleotide-
7	478.5	11.8	962	2	potassium channel
8	473.5	11.7	1174	2	potassium channel
9	472	11.7	690	1	CGMP-gated ion cha
10	465.5	11.5	691	2	rod cyclic nucleot
11	465	11.5	663	2	CGMP-gated channel
12	463.5	11.5	645	2	alpha subunit of r
13	462	11.4	732	2	cyclic nucleotide-
14	459.5	11.4	682	1	cyclic nucleotide-
15	459	11.4	909	2	CGMP-gated cation
16	454	11.2	688	2	CGMP-gated cation
17	452	11.2	989	2	potassium channel
18	449.5	11.1	575	2	olfactory cyclic n
19	447	11.1	1087	2	probable potassium
20	445.5	11.0	665	2	DnMGC protein - f
21	445.5	11.0	686	1	CGMP-gated ion cha
22	444	11.0	1284	2	probable potassium
23	438.5	10.9	514	2	hypothetical prote
24	432.5	10.7	690	2	CGMP-gated cation
25	409	10.1	1102	2	potassium channel
26	402.5	10.0	772	2	hypothetical prote
27	400.5	9.9	934	2	potassium channel
28	396.5	9.8	828	2	potassium channel
29	375	9.3	787	2	potassium channel

30	361	8.9	800	2	T19627	hypothetical prote
31	337	8.3	733	2	E85357	hypothetical prote
32	335	8.3	690	2	G84638	hypothetical prote
33	330.5	8.2	838	2	S23606	potassium channel
34	330.5	8.2	857	2	S62694	potassium channel
35	328	8.1	747	2	T52572	cyclic nucleotide
36	328	8.1	887	2	T03939	potassium channel
37	327.5	8.1	883	2	T07651	potassium channel
38	323.5	8.0	746	2	H86330	probable cyclic nu
39	322	8.0	706	2	F86143	hypothetical prote
40	321.5	8.0	726	2	A85355	hypothetical prote
41	320	7.9	807	2	T12177	potassium channel
42	319.5	7.9	673	2	T20936	hypothetical prote
43	317	7.9	677	2	S32816	potassium channel
44	317	7.9	710	2	T52573	cyclic nucleotide
45	313	7.8	716	2	T51354	cyclic nucleotide-

ALIGNMENTS

RESULT 1

I38465
probable potassium channel subunit - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C:Accession: I38465
R:Warme, J.W.; Ganetzky, B.
Proc. Natl. Acad. Sci. U.S.A. 91, 3438-3442, 1994
A:Title: A family of potassium channel genes related to eag in Drosophila and mammals.
A:Reference number: A54953; MUID:94211879; PMID:8159766
A:Accession: I38465
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1159 <RES>
A:Cross-references: UNIPROT:Q12809; UNIPARC:UPI0000062255; EMBL:U04270; NID:9487737; PID:
F:742-858/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 12.7%; Score 512.5; DB 2; Length 1159;

Best Local Similarity 24.2%; Pred. No. 1.2e-24;

Matches 208; Conservative 124; Mismatches 322; Indels 205; Gaps 34;

QY	3	AEORPAAGSEGNATPGLEAV-PPVAPP-----ATAASGPIPKSG-----PEPKRHL 49
DB	277	ASVRRASSADD-----IEAMRAGVLPPPPRHASTGAMHPL-RSGLLNSTSDSLVRYRTI 330
QY	50	GTLLQPTVNFKSLRVFG-----SHKAVEIEQERKVSAGA-----83
DB	331	SKIPQITLNFVDLK--GDPFLASPTSDRIIAPKIKERTHNVTI-KVTQVLSLGADVLP 387
QY	84	-----WIHPYSDFRPFYWDLIMLLMVGNLIVLPVGITFF---KEENSP-----124
DB	388	YKLOAPRIHRWTLHYSPFKAVMDLILLVIYVFTPYSAAPFLKETEEGPPATECGY 447
QY	125	---PWIVFNVLSDTFLLDLVNFRCIVVEGAEILLAPRAIRTYRLTWFLVDLISSI 181
DB	448	ACQPLAVDLVIDIMFIVDILNFRFT--TYVNANEEVSHPGRIAVHYFKGFWLIDVMAAI 506
QY	182	PVDYIFLVVELEPRLDAEVYKTARALIRVFTKILSLRLRLSLIRYIHOEEIFHMT 241
DB	507	PFLLIFGSGSEBLIG--LKTRALLRLVRAR-----KLDRIYSEY-----545
QY	242	YDLASAVRIFNLIENMLLCHWDGCLQFLVPMLOFPDPDPCWVSINHMVNHSGROYSH- 300
DB	546	---GRAV--LFLMCTCFALIAHMLACIWAIGNMEQPHMDSRIGLWLNLDGQIGKPNSS 600
QY	301	-----ALPKAMSHMLCICYGOQAPVGMGPDVWLTMLSMIVGATCYAMFCHAT 347
DB	601	GLGGPSIKDKYVTALYFTFSSLTSGVGNVSPNTSEKIFISICVMLGISLMAVIFGNVS 660
QY	348	ALTQSLDSSRRQYQEKYQVQYMSFKLPADFRQRIHEYHYEHRYQ-GKMFDEESILGEL 406
DB	661	AIIOQLRYSGTARYHTQMLRVREFIRFHQPNPVRQRLSEYFQHAWSYTGIDNNAVLKGF 720

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 26, 2006, 20

Title: US-09-767-597-1
Perfect score: 4038
Sequence: 1 MEAEQRPAGASEGA

Scoring table: BLOSUM62
Gapop 10.0, Gape

Searched: 2849598 seqs, 925

Total number of hits satisfying c

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45

Database: UniProt 2.2.2
1: uniprot_sprot
2: uniprot_trem

Pred. No. is the number of
score greater than or equal
and is derived by analysis

Result No.	Score	Query Match	Length	DB
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2	4027	99.7	774	2
3	3806.5	94.3	779	1
4	3780	93.6	780	1
5	2567.5	63.6	1175	1
6	2541.5	62.9	1198	1
7	2540	62.9	1203	1
8	2455.5	60.8	1186	1
9	2402	59.5	889	1
10	2396	59.3	863	1
11	2391.5	59.2	863	1
12	2384	59.0	1604	2
13	2373	58.8	838	2
14	2361	58.5	1512	2
15	2339.5	57.9	822	1
16	2335	57.8	890	1
17	2325	57.6	890	2
18	2317	57.4	910	1
19	2316	57.4	910	1
20	2275	56.3	938	2
21	2121.5	52.5	971	2
22	1997	49.5	890	2
23	1731.5	42.9	678	2
24	1702	42.1	674	2
25	1699.5	42.1	691	2
26	1695.5	42.0	618	2
27	1695.5	42.0	627	2
28	1695.5	42.0	1282	2
29	1695.5	42.0	1290	2
30	1694	42.0	945	2
31	1688.5	41.8	632	2

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Q96777_HELVI
Q7QK47_ANOGA
Q6WL05_PANAR
Q56JH9_DROME
Q56JH8_DROME
Q56JH7_DROME
Q2PDN3_DROME
Q9YIJ9_DROME
Q6WL04_APEME

Q4SQC3_tetraodon n
Q96777_heliethis v
Q7QK47_anopheles g
Q6WL05_panulirus a
Q56JH9_drosophila
Q56JH8_drosophila
Q56JH7_drosophila
Q2PDN3_drosophila
Q9YIJ9_drosophila
Q6WL04_apls mellif

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield I.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Putative hyperpolarization-activated ion channel
exhibiting weak selectivity for potassium over sodium ions (By

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

Q56JH7_drosophila
Q2PDN4_drosophila
Q5XQT6_apls mellif
Q76977_strongyloce
Q48DA7_tetraodon n
Q80Z66_cavia porce
Q45ZV2_strongyloce

32 1676 41.5 1319 2 Q56JH7_DROME
33 1676 41.5 1327 2 Q2PDN4_DROME
34 1670.5 41.4 664 2 Q5XQT6_APEME
35 1544.5 38.2 767 2 Q76977_STRPU
36 1491.5 36.9 594 2 Q48DA7_TETNG
37 1422 35.2 318 2 Q80Z66_CAVPO
38 1135.5 28.1 638 2 Q45ZV2_STRPTI

273 PMLQDFPDCWVSINHMVNSWGROXSHALFKAMSHMLCIGYGOQAPVGMEDVWLTMLSM 332
 346 PMLQDFPDCWVSINHMVNSWGROXSHALFKAMSHMLCIGYGOQAPVGMEDVWLTMLSM 405
 333 IVGATCYAMFICHATALIQLSDSSRRQYQEKYQVEQYMSFHKLPADTRQRIHEYYEHRY 392
 406 IVGATCYAMFICHATALIQLSDSSRRQYQEKYQVEQYMSFHKLPADTRQRIHEYYEHRY 465
 393 QGKMFDEESILGELSEPLREIINFCTCRGLVAHMLPFAHADPSFVAVLTKLRFVFPQ 452
 466 QGKMFDEESILGELSEPLREIINFCTCRGLVAHMLPFAHADPSFVAVLTKLRFVFPQ 525
 453 DLVVRGSGRKMVFIOHGLLSVLARGARDTRITDGSYFGEICLLTRGRRTASVRADTYC 512
 526 DVIIRREGTIGKMYFIOHGVVSVLTGKNETKLADGSYFGEICLLTRGRRTASVRADTYC 585
 513 RLYSLSDVHFNVALEEFPMRRAPFETVAMDRLLRIGKNSILQKRSPPSGSSGIME- 571
 586 RLYSLSDVNFNEVLEEYPMRRAPFETVALDRLDRIGKNSILHVKVQHDLSNGVFNQEN 645
 572 ---OHLVQHDMDRMAHVRGAPSTGAQLSGKPLWEPLVHAPLOAAVTSNVAIALTHOR 628
 646 EIIQIIVQHDREMAHVRGAPSTGAQLSGKPLWEPLVHAPLOAAVTSNVAIALTHOR 704
 629 GPLPLSPDPSATLL---ARSAMRSAGSPASP-----LVPVRAG---PWASTSRPLPAP 674
 705 -----PRLPAAIFRPPPGSGLNLGAGQTPRHLKRLQSLIPSLGASPASSPSQVDT 758
 675 PARTLH-----ASLSR-AGRSQV---SLLGPPPPGGG-----R 703
 759 SSSSFHIQQLAGFAPAGLSPLLPSSSSPPPGACGSPSAPTSGAGVAATTIAGFGPHK 818
 704 RLQ-----PRGRPLSASOPS-LPQRATG-----DGSP 729
 819 ALGGLSSSDSPLLTLPQPGARSPOAAQSPAPPGARGGLGLPEHFLPPPPSSRSPSSP 878
 730 GRKGSGERLPPS---GLLAKPPRTAQ-PPRPVP-----EPA--TPRG 767
 879 GOLQO-----PPGELSLGLATGPLSTPTETPPRQPEPPLVAGASGASPVGTFRG 929

RESULT 2

US-09-949-016-6615
 ; Sequence 6615, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; PRIOR FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6615
 ; LENGTH: 1203
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-6615

Query Match 62.9%; Score 2540; DB 2; Length 1203;
 Best Local Similarity 59.6%; Pred. No. 2,7e-217;
 Matches 534; Conservative 72; Mismatches 144; Indels 146; Gaps 19;
 4 EORPAAGASGATPPGLEAVPPVAPPATAASGPIPKSGPEPK-----45
 142 DRTTPGLAAEPERPGASQAAPASPPPPPPQPPQPPASASCEQPSVDTAIVKGGAAAGDQIL 201

46 -----RRHLGTLLOPTVNKESLAVFGSHKAVEIEORVKSAGAMIHPYSDF 92
 202 PEAEVRLGOAGFMQKQFAGMLQPGVNFSLRMPFSQKAVEIEORVKSAGAMIHPYSDF 261
 93 RPYMDLIMLLMVGNLIVLPVGIITPFKEENSPPMVFNVLSDTFFLLDLVNFRTGIVVE 152
 262 RPYMDLIMLLMVGNLIIIPVGIITPFKEENSPPMVFNVLSDTFFLLDLVNFRTGIVVE 321
 153 EQAEILLAPRAIRTRYLTWFLVDLISSIPVDYIPLVVELEPRDLDAEYKTKARALRIVRF 212
 322 DNTIELDQRIKMKYLSWFMVDFISSIPVDYIPLV--ETRIDSEYKTKARALRIVRF 379
 213 TKILSLRLRLSLRIYIHOWEIEFHMTYDILASAVRIENLIGNMLLLCHWDGCLQFLV 272
 380 TKILSLRLRLSLRIYIHOWEIEFHMTYDILASAVRIENLIGNMLLLCHWDGCLQFLV 439
 273 PMLQDFPDCWVSINHMVNSWGROXSHALFKAMSHMLCIGYGOQAPVGMEDVWLTMLSM 332
 440 PMLQDFPDCWVSINHMVNSWGROXSHALFKAMSHMLCIGYGOQAPVGMEDVWLTMLSM 499
 333 IVGATCYAMFICHATALIQLSDSSRRQYQEKYQVEQYMSFHKLPADTRQRIHEYYEHRY 392
 500 IVGATCYAMFICHATALIQLSDSSRRQYQEKYQVEQYMSFHKLPADTRQRIHEYYEHRY 559
 393 QGKMFDEESILGELSEPLREIINFCTCRGLVAHMLPFAHADPSFVAVLTKLRFVFPQ 452
 560 QGKMFDEESILGELSEPLREIINFCTCRGLVAHMLPFAHADPSFVAVLTKLRFVFPQ 619
 453 DLVVRGSGRKMVFIOHGLLSVLARGARDTRITDGSYFGEICLLTRGRRTASVRADTYC 512
 620 DVIIRREGTIGKMYFIOHGVVSVLTGKNETKLADGSYFGEICLLTRGRRTASVRADTYC 679
 513 RLYSLSDVHFNVALEEFPMRRAPFETVAMDRLLRIGKNSILQKRSPPSGSSGIME- 571
 680 RLYSLSDVNFNEVLEEYPMRRAPFETVALDRLDRIGKNSILHVKVQHDLSNGVFNQEN 739
 572 ---OHLVQHDMDRMAHVRGAPSTGAQLSGKPLWEPLVHAPLOAAVTSNVAIALTHOR 628
 740 EIIQIIVQHDREMAHVRGAPSTGAQLSGKPLWEPLVHAPLOAAVTSNVAIALTHOR 798
 629 GPLPLSPDPSATLL---ARSAMRSAGSPASP-----LVPVRAG---PWASTSRPLPAP 674
 799 -----PRLPAAIFRPPPGSGLNLGAGQTPRHLKRLQSLIPSLGASPASSPSQVDT 852
 675 PARTLH-----ASLSR-AGRSQV---SLLGPPPPGGG-----R 703
 853 SSSSFHIQQLAGFAPAGLSPLLPSSSSPPPGACGSPSAPTSGAGVAATTIAGFGPHK 912
 704 RLQ-----PRGRPLSASOPS-LPQRATG-----DGSP 729
 913 ALGGLSSSDSPLLTLPQPGARSPOAAQSPAPPGARGGLGLPEHFLPPPPSSRSPSSP 972
 730 GRKGSGERLPPS---GLLAKPPRTAQ-PPRPVP-----EPA--TPRG 767
 973 GOLQO-----PPGELSLGLATGPLSTPTETPPRQPEPPLVAGASGASPVGTFRG 1023

RESULT 3

US-10-067-457-3
 ; Sequence 3, Application US/10067457
 ; Patent No. 6979532
 ; GENERAL INFORMATION:
 ; APPLICANT: Aventis Pharma Deutschland GmbH
 ; TITLE OF INVENTION: Process for identifying substances which modulate the
 ; activity of hyperpolarization-activated cation channels
 ; FILE REFERENCE: AVE D-2000/A006
 ; CURRENT APPLICATION NUMBER: US/10/067,457
 ; PRIOR FILING DATE: 2002-04-09
 ; PRIOR APPLICATION NUMBER: US/09/779,587
 ; PRIOR FILING DATE: 2001-02-09
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: PatentIn Ver. 2.1

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 26, 2006, 20:22:41 ; Search time 53 Seconds
(without alignments)
1278.277 Million cell updates/sec

Title: US-09-767-597-1

Perfect score: 4038

Sequence: 1 MEAEQRPAAGASEGATPGLE.....PRPPVPEPATRGLQLSANM 774

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum-Match 100%

Ligging flvst 45 summaries

Database :

Issued patents AA.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5 COMB.pcp.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6 COMB.pcp.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pcp.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pcp.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pcp.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pcp.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfilese1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2540	62.9	1109	2	US-09-949-016-10771
2	2540	62.9	1203	2	US-09-949-016-6615
3	2540	62.9	1203	2	US-10-067-457-3
4	2402	59.5	855	2	US-09-949-016-7263
5	2402	59.5	889	2	US-09-949-016-6036
6	2402	59.5	889	2	US-10-067-457-1
7	2391.5	59.2	863	2	US-10-067-457-5
8	2316	57.4	910	2	US-08-997-685A-2
9	2316	57.4	910	2	US-08-997-685A-3
10	2251	55.7	597	2	US-09-086-436-41
11	2248	55.7	597	2	US-08-997-685A-12
12	2216	54.9	749	2	US-08-997-685A-10
13	2216	54.9	749	2	US-09-086-436-39
14	2202.5	54.5	504	2	US-09-086-436-33
15	2199.5	54.5	528	2	US-08-997-685A-4
16	2154	53.3	506	2	US-08-997-685A-6
17	2143	53.1	506	2	US-09-086-436-35
18	858.5	21.3	308	2	US-09-270-767-32667
19	858.5	21.3	308	2	US-09-270-767-47884
20	524	13.0	1017	2	US-09-600-776-6
21	524	13.0	1017	2	US-09-965-830-6
22	512.5	12.7	905	2	US-10-104-047-2728
23	512.5	12.7	1159	1	US-08-956-242-13
24	512.5	12.7	1159	2	US-09-351-215-13
25	512.5	12.7	1159	2	US-09-226-012-2
26	512.5	12.7	1159	2	US-09-226-012-4

27	512.5	12.7	1159	2	US-09-358-383C-10	Sequence 10, Appl
28	512.5	12.7	1159	2	US-09-275-252A-12	Sequence 12, Appl
29	509	12.6	131	2	US-08-997-685A-45	Sequence 45, Appl
30	505	12.5	119	2	US-08-997-685A-53	Sequence 53, Appl
31	493.5	12.2	694	2	US-09-538-092-1351	Sequence 1351, Ap
32	493.5	12.2	698	2	US-09-949-016-10215	Sequence 3, Appl
33	486.5	12.0	962	2	US-09-694-777A-3	Sequence 9, Appl
34	485	12.0	962	2	US-09-614-480-9	Sequence 9, Appl
35	485	12.0	962	2	US-10-422-075-9	Sequence 9, Appl
36	481.5	11.9	960	2	US-09-694-777A-21	Sequence 21, Appl
37	477	11.8	989	2	US-09-694-777A-4	Sequence 4, Appl
38	476.5	11.8	962	2	US-09-694-777A-24	Sequence 24, Appl
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40	475.5	11.8	988	2	US-10-162-012-5	Sequence 5, Appl
41	475.5	11.8	988	2	US-10-422-075-2	Sequence 2, Appl
42	474	11.7	988	2	US-10-162-012-12	Sequence 12, Appl
43	472	11.7	987	2	US-09-694-777A-22	Sequence 22, Appl
44	466	11.5	909	2	US-09-538-092-1315	Sequence 1315, Ap
45	456.5	11.3	575	2	US-09-927-267-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-949-016-10771
; Sequence 10771, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10771

; LENGTH: 1109

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-10771

Query Match 62.9%; Score 2540; DB 2; Length 1109;
Best Local Similarity 59.8%; Pred. No. 2.4e-217;
Matches 534; Conservative 72; Mismatches 144; Indels 146; Gaps 19;

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DB	48	DRTPGLAAEPERPGASQAAPSPPPQPPQPPASASCEQPSVDTAIKVEGGAAGDQIL	107
QY	46	-----RRHLGTLLOFTVNFKSLRVFGSKHVEIQEVRKSGAGWIIHPYSDF	92
DB	108	PEAEVRLGQAGFMQRQGMALQGVNKFSLRMFGSQKAVEREQERVKSAGWIIHPYSDF	167
QY	93	RFVWDLMLLLMGNLIVLPVGTTFPKKEENSPWIVNFVLSDTFFLLDLVLFNRTGIWE	152
DB	168	RFVWDLTMLLLMGNLIIIPVGTTFPKKENTTTWIVNFVVSDFFLDLVLFNRTGIWE	227
QY	153	EGAEILLAPRAIRTYLRTWFLVDLIISSIPVDYIFLWVELEPRLDAAVYKATARIVRF	212
DB	228	DNTEILLDPQRIKKYKSKFWFDFISSIPVDYIFLIV--ETRIDSEVYKATARIVRF	285
QY	213	TKILSLRLRLRLRLRYIYHQWEEIFHMTYDLSAVVRIFNLIGMMLLLCHWDGCLQFLV	272
DB	286	TKILSLRLRLRLRLRYIYHQWEEIFHMTYDLSAVVRIVNLIGMMLLLCHWDGCLQFLV	345

Db 301 ALFKAMSHMLCIGYQQAPVGMDFVMTLMSIVGATCYAMFIGHATATLIQSLDSSRQY 360
 QY 361 QEKYKQVEQYMSFKHKLPAIDTRQRIHEYYEHRYGKMFDEESILGELSEPLREBIINFTCR 420
 Db 361 QEKYKQVEQYMSFKHKLPAIDTRQRIHEYYEHRYGKMFDEESILGELSEPLREBIINFTCR 420
 QY 421 GLVAHMLPLFAHADPSFVTAULTKLRFEVFGDLVVRGSGVGRKMYFIQHGLLSVLARGA 480
 Db 421 GLVAHMLPLFAHADPSFVTAULTKLRFEVFGDLVVRGSGVGRKMYFIQHGLLSVLARGA 480
 QY 481 RDTLTDGSGYFGEICLLTRGRRTASVRADTYCRLYSLSDVDFHNAVLSEFPMMRRAPETVA 540
 Db 481 RDTLTDGSGYFGEICLLTRGRRTASVRADTYCRLYSLSDVDFHNAVLSEFPMMRRAPETVA 540
 QY 541 MDRLIRIGKKNSTLORKESEPSGSGGIMEQHLVQHDRDMARGVRGRAPSTGAQLSGKP 600
 Db 541 MDRLIRIGKKNSTLORKESEPSGSGGIMEQHLVQHDRDMARGVRGRAPSTGAQLSGKP 600
 QY 601 VLWEPLVHAPLOAAAVTSNVAIALTHORGPLPLSPDPSATLLARSAMRSAGSPASPLVPV 660
 Db 601 VLWEPLVHAPLOAAAVTSNVAIALTHORGPLPLSPDPSATLLARSAMRSAGSPASPLVPV 660
 QY 661 RAGWASTSRPLPAPPARTLHASLSRAGSQVSLGPPGCGRRLLGPRGRPLSASQPSLP 720
 Db 661 RAGWASTSRPLPAPPARTLHASLSRAGSQVSLGPPGCGRRLLGPRGRPLSASQPSLP 720
 QY 721 ORATGDSGPRKSGSERLPPSGLLAKPRTAQPRTAQPRTAQPRTAQPRTAQPRTAQPRTA 774
 Db 721 ORATGDSGPRKSGSERLPPSGLLAKPRTAQPRTAQPRTAQPRTAQPRTAQPRTAQPRTA 774

RESULT 2

US-10-158-684-10
 ; Sequence 10, Application US/10158684
 ; Publication No. US20030022812A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chaplan, Sandra
 ; APPLICANT: Liu, Changlu
 ; APPLICANT: Lee, Doo Hyun
 ; APPLICANT: Dubin, Adrienne
 ; APPLICANT: Guo, Hong-Qing
 ; APPLICANT: Luo, Lin
 ; APPLICANT: Brown, Sean
 ; TITLE OF INVENTION: Treating Pain by Targeting Hyperpolarization-Activated Cyclic
 ; FILE REFERENCE: Nucleotide-Gated Channels
 ; CURRENT APPLICATION NUMBER: US/10/158,684
 ; CURRENT FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: 60/297,108
 ; PRIOR FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: 60/347,945
 ; PRIOR FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 10
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-158-684-10

Query Match 100.0%; Score 4038; DB 4; Length 774;
 Best Local Similarity 100.0%; Pred. No. 1.1e-282;
 Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEAEORPAAGASGATGLENVPPVAPPATTAASGPIKSGPEPKRHLGTLLOPTVNF 60
 Db 1 MEAEORPAAGASGATGLENVPPVAPPATTAASGPIKSGPEPKRHLGTLLOPTVNF 60
 QY 61 SLRVFGSHKAVETQERVKASAGAWIHPYSDFRFYWDLMMLMGNLIVLPVGTTFKE 120
 Db 61 SLRVFGSHKAVETQERVKASAGAWIHPYSDFRFYWDLMMLMGNLIVLPVGTTFKE 120
 QY 121 ENSPPWIVFNLSDTFFLLDLVLFNRTGIVVEGAEILLAPRAIRYLRTRTWFLVDLISS 180
 Db 121 ENSPPWIVFNLSDTFFLLDLVLFNRTGIVVEGAEILLAPRAIRYLRTRTWFLVDLISS 180

QY 181 IPVDYIFLVLEPRDLAEVYKTARALRIVRPTKILSLRLRLRLRLRLRLRLRLRLRLRLRLRL 240
 Db 181 IPVDYIFLVLEPRDLAEVYKTARALRIVRPTKILSLRLRLRLRLRLRLRLRLRLRLRLRLRL 240
 QY 241 TYDLASAVVRIFNLIGMMLLCHWDGCLQFLVPMQLQDPFPPDCWVSINHMVHNSWGRQYSH 300
 Db 241 TYDLASAVVRIFNLIGMMLLCHWDGCLQFLVPMQLQDPFPPDCWVSINHMVHNSWGRQYSH 300
 QY 301 ALFKAMSHMLCIGYQQAPVGMDFVMTLMSIVGATCYAMFIGHATATLIQSLDSSRQY 360
 Db 301 ALFKAMSHMLCIGYQQAPVGMDFVMTLMSIVGATCYAMFIGHATATLIQSLDSSRQY 360
 QY 361 QEKYKQVEQYMSFKHKLPAIDTRQRIHEYYEHRYGKMFDEESILGELSEPLREBIINFTCR 420
 Db 361 QEKYKQVEQYMSFKHKLPAIDTRQRIHEYYEHRYGKMFDEESILGELSEPLREBIINFTCR 420
 QY 421 GLVAHMLPLFAHADPSFVTAULTKLRFEVFGDLVVRGSGVGRKMYFIQHGLLSVLARGA 480
 Db 421 GLVAHMLPLFAHADPSFVTAULTKLRFEVFGDLVVRGSGVGRKMYFIQHGLLSVLARGA 480
 QY 481 RDTLTDGSGYFGEICLLTRGRRTASVRADTYCRLYSLSDVDFHNAVLSEFPMMRRAPETVA 540
 Db 481 RDTLTDGSGYFGEICLLTRGRRTASVRADTYCRLYSLSDVDFHNAVLSEFPMMRRAPETVA 540
 QY 541 MDRLIRIGKKNSTLORKESEPSGSGGIMEQHLVQHDRDMARGVRGRAPSTGAQLSGKP 600
 Db 541 MDRLIRIGKKNSTLORKESEPSGSGGIMEQHLVQHDRDMARGVRGRAPSTGAQLSGKP 600
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 Db 601 VLWEPLVHAPLOAAAVTSNVAIALTHORGPLPLSPDPSATLLARSAMRSAGSPASPLVPV 660
 QY 661 RAGWASTSRPLPAPPARTLHASLSRAGSQVSLGPPGCGRRLLGPRGRPLSASQPSLP 720
 Db 661 RAGWASTSRPLPAPPARTLHASLSRAGSQVSLGPPGCGRRLLGPRGRPLSASQPSLP 720
 QY 721 ORATGDSGPRKSGSERLPPSGLLAKPRTAQPRTAQPRTAQPRTAQPRTAQPRTAQPRTA 774
 Db 721 ORATGDSGPRKSGSERLPPSGLLAKPRTAQPRTAQPRTAQPRTAQPRTAQPRTAQPRTA 774

RESULT 3

US-10-158-711-10
 ; Sequence 10, Application US/10158711
 ; Publication No. US20030022813A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chaplan, Sandra
 ; APPLICANT: Liu, Changlu
 ; APPLICANT: Lee, Doo Hyun
 ; APPLICANT: Dubin, Adrienne
 ; APPLICANT: Guo, Hong-Qing
 ; APPLICANT: Luo, Lin
 ; APPLICANT: Brown, Sean
 ; TITLE OF INVENTION: Treating Pain by Targeting Hyperpolarization-Activated Cyclic
 ; FILE REFERENCE: Nucleotide-Gated Channels
 ; CURRENT APPLICATION NUMBER: US/10/158,711
 ; CURRENT FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: 60/297,108
 ; PRIOR FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: 60/347,945
 ; PRIOR FILING DATE: 2001-11-07
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 774
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-158-711-10
 Query Match 100.0%; Score 4038; DB 4; Length 774;
 Best Local Similarity 100.0%; Pred. No. 1.1e-282;
 Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

28	2333	57.8	890	5	US-10-466-992-8	Sequence 8, Appl
29	2333	57.8	890	5	US-10-466-992-12	Sequence 12, Appl
30	2332	57.8	890	5	US-10-466-992-4	Sequence 4, Appl
31	2332	57.6	890	5	US-10-466-992-6	Sequence 6, Appl
32	2325.9	57.6	890	4	US-10-466-992-8	Sequence 2, Appl
33	2321.5	57.5	887	4	US-10-296-270-2	Sequence 6, Appl
34	2317	57.5	910	5	US-10-466-992-21	Sequence 21, Appl
35	2316	57.4	910	3	US-09-086-436-31	Sequence 31, Appl
36	2316	57.4	910	4	US-10-753-991-31	Sequence 31, Appl
37	2316	57.4	910	5	US-10-384-107-2	Sequence 2, Appl
38	2316	57.4	910	5	US-10-466-992-22	Sequence 22, Appl
39	2314	57.3	890	4	US-10-311-795-2	Sequence 2, Appl
40	2298	56.9	998	5	US-10-466-992-23	Sequence 23, Appl
41	2251	55.7	597	3	US-09-086-436-41	Sequence 41, Appl
42	2251	55.7	597	4	US-10-753-991-41	Sequence 41, Appl
43	2248	55.7	597	5	US-10-384-107-12	Sequence 12, Appl
44	2216	54.9	749	3	US-09-086-436-39	Sequence 39, Appl
45	2216	54.9	749	4	US-10-753-991-39	Sequence 39, Appl

RESULT 1

1. Application US/09548933
 Application NO. US20030044889A1
 INFORMATION:
 INVENTOR: Timothy James
 AGENT: Jegla, Inc.
 AGENT: ICAGEN, Inc.
 PRIORITY INVENTION: Human HAC3
 REFERENCE: 018512-002210US
 APPLICATION NUMBER: US/09/548,933
 FILING DATE: 2000-04-13
 APPLICATION NUMBER: US 60/129,456
 FILING DATE: 1999-04-15
 OF SEQ ID NOS: 16
 E: PatentIn Ver. 2.1
 IO 1
 : 774
 PRT
 SM: Homo sapiens
 E:
 INFORMATION: human hyperpolarization-activated voltage-gated
 INFORMATION: cation channel 3 (HAC3)
 933-1

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/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: human hyperpolarization-activated voltage-gated
/ OTHER INFORMATION: cation channel 3 (HAC3)
US-09-548-933-1

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Result No.	Query Match	Score	Length	ID	Description
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2	4038	100.0	774	4	US-10-158-684-10	Sequence 10, Appl
3	4038	100.0	774	4	US-10-158-711-10	Sequence 10, Appl
4	4038	100.0	774	4	US-10-332-447-25	Sequence 25, Appl
5	3670	90.9	703	4	US-10-311-795-8	Sequence 8, Appl
6	2540	62.9	1203	4	US-10-067-457-3	Sequence 3, Appl
7	2540	62.9	1203	4	US-10-311-795-6	Sequence 6, Appl
8	2540	62.9	1245	4	US-10-276-774-2323	Sequence 2323, Ap
9	2402	59.5	889	4	US-10-067-457-1	Sequence 1, Appl
10	2402	59.5	889	4	US-10-311-795-4	Sequence 4, Appl
11	2402	59.5	889	5	US-10-756-149-5170	Sequence 5170, Ap
12	2394.5	59.2	863	4	US-10-067-457-5	Sequence 5, Appl
13	2391	59.2	875	3	US-09-548-933-15	Sequence 15, Appl
14	2350	58.2	882	5	US-10-343-903-11	Sequence 11, Appl
15	2346	58.1	882	4	US-10-768-158-38	Sequence 38, Appl
16	2346	58.1	890	4	US-10-158-684-4	Sequence 4, Appl
17	2346	58.1	890	4	US-10-158-711-4	Sequence 4, Appl
18	2346	58.1	890	4	US-10-296-270-4	Sequence 4, Appl
19	2346	58.1	890	4	US-10-287-226-352	Sequence 352, App
20	2345	58.1	837	5	US-10-466-993-20	Sequence 20, Appl
21	2344	58.0	890	5	US-10-466-992-16	Sequence 16, Appl
22	2341	58.0	890	4	US-10-296-270-8	Sequence 8, Appl
23	2341	58.0	890	5	US-10-466-992-10	Sequence 10, Appl
24	2340	57.9	890	5	US-10-466-992-2	Sequence 2, Appl
25	2340	57.9	890	5	US-10-466-992-14	Sequence 14, Appl
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132 LSTFFLLDLNFRGIVVEBGAELLLAPRAIRTRYLRTWFLVDLISSIPVDYIFLVE 191
209 SADVLVLDVLRARTGF-LEQGLMVSDTNRLWQHYYKTTQFKLDVLSVPTDLAYL--- 264
192 LEPRDLAEVVKTAARALIRVRETKILSLRLRLSLRIRYIHOWEEIFHMTYDLASAVRI 251
265 -----KVGNTNPEVRFN-----RLKFSRLFFEDRT-----TRTNPNMFR 303
252 FNLIGMMLLLCHWDGCLQFLVPMLODFPPDCWVSINHMV--NHSWGRQYSHALFKAMSHM 309
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310 LCIGYQQQAPVGMDFWLTWLSMIVGATCVAMPIGHATALIOSLSSRRQYQEKYQVBEQ 369
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423 YMQFRKVTQDLETRVTRWFDYLMANKTVDKEVLSKSLDKUAEIAINHLDTLKKVRI 482
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483 FQDCEAGLLVELVLRPTVFSFGDYICKGDIGKEMYIINEGKLAVADDGVTQFVLS 542
487 DGSYFGEICLL-----TGRRRTASVADTYCKLYSLSDVDFHNAVLEPPMRRAPETVA 540
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541 MDRLRAIGKNSILQKRSEP 561
603 RQILMKONLIDELARAGADP 623

RESULT 2

US-11-312-958-30
Sequence 30, Application US/11312958
Publication No. US20060100152A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Rosenfeld, Julie Beth
APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
TITLE OF INVENTION: 13424 MOLECULES
FILE REFERENCE: MPI02-027PIRNMNIM
CURRENT APPLICATION NUMBER: US/11/312,958
CURRENT FILING DATE: 2005-12-20
PRIOR APPLICATION NUMBER: US/10/369,022
PRIOR FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: US 60/360,495
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/370,121
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/373,010
PRIOR FILING DATE: 2002-04-16
PRIOR APPLICATION NUMBER: US 60/373,908
PRIOR FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US 60/377,717
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US 60/379,949
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US 60/382,409
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/385,280
PRIOR FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/386,879
PRIOR FILING DATE: 2002-06-06

Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 989
TYPE: PRT
ORGANISM: Homo sapiens
US-11-312-958-30
Query Match 11.8%, Score 477, DB 7, Length 989;
Best Local Similarity 23.0%, Pred. No. 1.6e-25;
Matches 192, Conservative 129, Mismatches 338, Indels 174, Gaps 27;
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QY 84 WIIHPYSDRFYFDWILMLLLMGNLIVLPVGITTFKEENSPPIVFNVLSDTFFLLDLVL 143
Db 209 IILH-YCVFKTTDWIILITFYTAILVPYVNSFKTRQNNVAVLVDSDIVDIFLVDIVL 267
QY 144 NFRGIVVEBGAELLLAPRAIRTRYLRTWFLVDLISSIPDYI-----FL----- 188
Db 268 NFHTTFVGPAG-EVISDPKLIRMYLKTWFVIDLSCLPYDVINAFENVVDSVAFMGDPG 326
QY 189 ----VVELEPRDLAEVVKTAARALIRVRETKILSLRLRLSLRIRYIHOWEEIFHMTYDL 244
Db 327 KIGFADQIPPPLEGRESQISSL-----FSS-LKVVRLRLRGVARKLDHYIE-----YGA 376
QY 245 ASAVVRIFNLIGMMLLLCHWDGCLQFLVPMLODFPPDCWVSINHMVNSWGRQ----- 297
Db 377 AVLVL-----LVCVFLAAHWMACIWSIGDYEIDED-----TKIRNNSWLQLAWDIGT 428
QY 298 -----YSHALFKAMSHMLCIGYQQQAPVGMDFWLTWLSMIVGA 336
Db 429 PYQFNGSGSGKWEKGPKNVYISLSYPTMTSLTSVGFNGIAPTDEIKIFAVALMIGS 488
QY 337 TCYAMFIGHTATALIQSLDSSRRQYQEKYQVQYMSFHLKPADTRORIEHYEYHRY-QGK 395
Db 489 LLYATIFGNVTTFQOMYANTNRHEMLNSVRDFELKYQVFKGLSERVMDIVSTWSMR 548
QY 396 MFDEESILGELSEPLREETINFTCRGLVAHMLPFAHADPSFVAVTLKLFVFOGDLV 455
Db 549 GIDTEKVLQICPKDMRADICVHLNRKVKEHPAFRLASDGCCLRALAMEFQTVHCAPGDLI 608
QY 456 VREGSVGRKMYFIQHGLLSVLARGARDTRLTDGSGYFGEICL--LTRGRTASVADTYCR 513
Db 609 YHAGESVDLSLCFVVGSGLEVIQDDVWAILGKGDVFGDFWKEATLAQSCANVRLTYCD 668
QY 514 LYSLSVDHFNVALEPPMRRAPF-----TVAMDRLRLRIGKNSI-----LQKRSEP 561
Db 669 LHVIKRDALQKLEFYAFSHSFERNLILTYNLKRIVFRKISDVKREEREMKRNAP 728
QY 562 ---SPGSSGGIMEQHLVQHDRDMARGVRGRAPSTGAQSLGKPKVLWEPVLVHAPLQAAVTS 618
Db 729 LILPPDHVRELFRFRQKEARLAERGGRDLDLDVEKGNVLTE---HASANHSLVKA 785
QY 619 NVAITALTHORGLPLSPDSPATILARSNWSRSGSPASPLVPVRAGPASTSLRLPAPPART 678
Db 786 SVVTV-----RESPATPVSFQA-----ASTSGVPD----- 810
QY 679 LHASLSRAGRQSVSLGPPGGGG---RRLGPRGRPL-----SASQPSLPOR- 722
Db 811 -HAKLOAPGS---ECLGPKGGGGCAKRSKWARFKDCKGSDWNKWSKASMETLPT 866
QY 723 -ATDGSFGRKSGSERLPPSGLL-----AKPRTAQPPRP-----PVPE 761
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RESULT 3

US-11-312-958-18
Sequence 18, Application US/11312958

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 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM protein - protein search, using sw model
 Run on: June 26, 2006, 20:39:42 ; Search time 23 Seconds
 (without alignments)
 768.802 Million cell updates/sec
 Title: US-09-767-597-1
 Perfect score: 4038
 Sequence: 1 MEAEQRPAGASEGATGPLE.....PRPVPEPATRGLQLSANM 774
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 99297 seqs, 22845552 residues
 Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications AA New.*
 1: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US09_NEW_PUB.pep.*
 2: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US06_NEW_PUB.pep.*
 3: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US07_NEW_PUB.pep.*
 4: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US08_NEW_PUB.pep.*
 5: /EMC_Celerra_SIDS3/prodata/2/pubpaa/PCT_NEW_PUB.pep.*
 6: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US10_NEW_PUB.pep.*
 7: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US11_NEW_PUB.pep.*
 8: /EMC_Celerra_SIDS3/prodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	493.5	12.2	694	7	US-11-302-678-26
2	477	11.8	989	7	Sequence 26, Appl
3	475.5	11.8	988	7	Sequence 30, Appl
4	331	8.2	694	6	Sequence 18, Appl
5	328.5	8.1	502	6	Sequence 52909, A
6	304.5	7.5	696	6	Sequence 52639, A
7	267.5	6.6	772	6	Sequence 47243, A
8	262	6.4	628	6	Sequence 53398, A
9	260	6.4	713	6	Sequence 43833, A
10	256.5	6.4	639	6	Sequence 45578, A
11	207	5.1	449	6	Sequence 5070, A
12	197	4.9	456	6	Sequence 23981, A
13	194	4.8	343	6	Sequence 30986, A
14	194	4.8	350	6	Sequence 43189, A
15	194	4.8	375	6	Sequence 19725, A
16	194	4.8	375	6	Sequence 19724, A
17	165.5	4.1	439	6	Sequence 22935, A
18	164.5	4.1	215	6	Sequence 36615, A
19	164	4.1	312	6	Sequence 19726, A
20	161	4.0	298	6	Sequence 22936, A
21	160	4.0	386	6	Sequence 22937, A
22	140.5	3.5	339	6	Sequence 53215, A
23	140	3.5	206	6	Sequence 34788, A
24	138	3.4	1327	7	Sequence 25833, A
25	136	3.4	461	6	Sequence 48, Appl
					Sequence 42292, A

Sequence 2847, Ap
 Sequence 1, Appli
 Sequence 20, Appl
 Sequence 2957, Ap
 Sequence 10919, A
 Sequence 42619, A
 Sequence 31470, A
 Sequence 45786, A
 Sequence 35037, A
 Sequence 2, Appli
 Sequence 17, Appl
 Sequence 27984, A
 Sequence 27983, A
 Sequence 44460, A
 Sequence 41294, A
 Sequence 31843, A
 Sequence 32616, A
 Sequence 14, Appl
 Sequence 34907, A

ALIGNMENTS

RESULT 1
 US-11-302-678-26
 ; Sequence 26, Application US/11302678
 ; Publication No. US20060088881A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals, Inc.
 ; APPLICANT: Silos-Santiago, Immaculada
 ; APPLICANT: Venkateswarlu, Karicheti
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
 ; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
 ; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
 ; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.
 ; FILE REFERENCE: MPI02-012PIRNM OMNI
 ; CURRENT APPLICATION NUMBER: US/11/302,678
 ; CURRENT FILING DATE: 2005-12-14
 ; PRIOR APPLICATION NUMBER: US/10/345,680
 ; PRIOR FILING DATE: 2003-01-16
 ; PRIOR APPLICATION NUMBER: US 60/349,511
 ; PRIOR FILING DATE: 2002-01-18
 ; PRIOR APPLICATION NUMBER: US 60/360,500
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/365,041
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 60/374,063
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/403,468
 ; PRIOR FILING DATE: 2002-08-14
 ; PRIOR APPLICATION NUMBER: US 60/414,262
 ; PRIOR FILING DATE: 2002-09-27
 ; PRIOR APPLICATION NUMBER: US 60/419,986
 ; PRIOR FILING DATE: 2002-10-21
 ; PRIOR APPLICATION NUMBER: US 60/423,809
 ; PRIOR FILING DATE: 2002-11-05
 ; PRIOR APPLICATION NUMBER: US 60/429,797
 ; PRIOR FILING DATE: 2002-11-26
 ; NUMBER OF SEQ ID NOS: 66
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 26
 ; LENGTH: 694
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-11-302-678-26

Query Match 12.2%; Score 493.5; DB 7; Length 694;
 Best Local Similarity 26.5%; Pred. No. 7.5e-27;
 Matches 133; Conservative 106; Mismatches 223; Indels 39; Gaps 10;
 QY 74 EORVKSAGAWIHPYSDRFRFYNDLIMLLMGNLIVLPVGITF--FKRENSPPMIVFNV 131

November 2005

Published Applications Nucleic Acid and Published Applications Amino Acid database searches now generate two sets of results each. The Published Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published Applications New databases; older published applications make up the Published Applications Main databases.

Searches run against Nucleic Acid Published Applications produce two sets of results, with the extensions **.rnpbm** (Published Applications NA_Main) and **.rnpbn** (Published Applications_NA_New). Searches run against Amino Acid Published Applications produce two sets of results, with the extensions **.rapbm** (Published Applications_AA_Main) and **.rapbn** (Published Applications_AA_New).